

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	1059	99.8	199	6	AA019413	Abb99462 Amino aci	
2	1048	98.8	487	5	AB017374	Human ret	
3	1048	98.8	666	6	ABU02087	Novel hum	
4	1048	98.8	667	4	AAU04557	Human str	
5	1048	98.8	667	4	AAAB8852	Human hyd	
6	1048	98.8	667	5	AAU83631	Human PRO	
7	1048	98.8	667	5	AAU78575	Human PRO	
8	1048	98.8	667	5	AAO19413	Human mol	
9	1048	98.8	667	6	ADA54816	Human PRO	
10	1048	98.8	667	6	ABU80778	Human PRO	
11	1048	98.8	667	6	ABO33744	Novel hum	
12	1048	98.8	667	6	ABJ72267	Human PRO	
13	1048	98.8	667	6	ABJ72395	Human PRO	
14	1048	98.8	667	6	ABO34290	Human sec	
15	1048	98.8	667	7	ABJ72097	Human mem	
16	1048	98.8	667	7	ADB83570	Novel hum	
17	1048	98.8	667	7	ADB80676	Novel hum	
18	1048	98.8	667	7	ADB73217	Novel hum	
19	1048	98.8	667	7	ADB78299	Novel hum	
20	1048	98.8	667	7	ADB84947	Human PRO	
21	1048	98.8	667	7	ADB78053	Novel hum	
22	1048	98.8	667	7	ADB87119	Human PRO	
23	1048	98.8	667	7	ADB84701	Human PRO	
24	1048	98.8	667	7	ADB83816	Novel hum	
25	1048	98.8	667	7	ADB72971	Novel hum	

CC bind immunospecifically to these sequences for therapeutic and diagnostic
CC applications. hSTRa6 nucleic acid fragments may be used as hybridization
CC probes to identify hSTRa6-encoding nucleic acids, or as PCR primers for
CC amplification and/or mutation of hSTRa6 molecules
XX
SQ Sequence 199 AA;

Query Match 99.8%; Score 1059; DB 6; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.8e-107; Indels 0; Gaps 0;
Matches 199; Conservative 0; Mismatches 0;
QY 1 MSQAGNOTSPGATEDSYSGSWYIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60
DB 1 MSQAGNOTSPGATEDSYSGSWYIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60
QY 61 LVLLLLAMLVRRRQLWPCVCRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCILLPDE 120
DB 61 LVLLLLAMLVRRRQLWPCVCRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCILLPDE 120
QY 121 DALPFLTTLASAPSDGKTEAPRGANKILGLFHYAALYPLAACATAGHTAAHLGSLTJW 180
DB 121 DALPFLTTLASAPSDGKTEAPRGANKILGLFHYAALYPLAACATAGHTAAHLGSLTJW 180
QY 181 AHLGVQVWQRAECPOVPKI 199
DB 181 AHLGVQVWQRAECPOVPKI 199

RESULT 2
AAO17374
ID AAO17374 standard; protein; 487 AA.
XX
AC AAO17374;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human retinoic acid responsive protein 53-57.
XX
KW Human; retinoic acid responsive protein 53.57; arrhythmia;
KW bronchial asthma; peptic ulcer; diabetes; cancer; cytostatic; antiulcer;
KW antiasthmatic; antidiabetic; endocrine; cardiant;
KW embryonic development disorder; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200226808-A1.
XX
PD 04-APR-2002.
XX
PF 20-AUG-2001; 2001WO-CN001252.
XX
PR 23-AUG-2000; 2000CN-00119715.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-330093/36.
DR N-PSDB; AAL45968.
XX
PT Human retinoic acid responsive protein 53.57 and encoding polynucleotide,
PT used in diagnosis and treatment of diseases e.g., arrhythmia, asthma,
PT diabetes and cancer.
XX
PS Claim 1; Page 32-33; 37pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC retinoic acid responsive protein 53.57. The sequences can be used in the
CC treatment of arrhythmia, bronchial asthma, peptic ulcer, diabetes, cancer
CC and embryonic development disorders. The present sequence is the protein
CC of the invention
XX
SQ Sequence 487 AA;

Query Match 98.8%; Score 1048; DB 5; Length 487;
Best Local Similarity 99.0%; Pred. No. 8.8e-106; Indels 0; Gaps 0;
Matches 196; Conservative 1; Mismatches 1;
QY 2 SOPAGNOTSPGATEDSYSGSWYIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSI 61
DB 3 SOPAGNOTSPGATEDSYSGSWYIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSI 62
QY 62 VLLLLAMLVRRRQLWPCVCRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCILLPDE 121
DB 63 VLLLLAMLVRRRQLWPCVCRGRPLSPVDFLAGDRPRAVPAAVFMVLLSSLCILLPDE 122
QY 122 ALPFLTTLASAPSDGKTEAPRGANKILGLFHYAALYPLAACATAGHTAAHLGSLTJW 181
DB 123 ALPFLTTLASAPSDGKTEAPRGANKILGLFHYAALYPLAACATAGHTAAHLGSLTJW 182
QY 182 HLGQVWQRAECPOVPKI 199
DB 183 HLGQVWQRAECPOVPKI 200

RESULT 3
ABU82087
ID ABU82087 standard; protein; 666 AA.
XX
AC ABU82087;
XX
DT 26-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10282.
XX
KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN US2003088063-A1.
XX
PD 08-MAY-2003.
XX
PF 12-AUG-2002; 2002US-00219003.
XX
PR 25-JUL-2000; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-393229/37.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 80; 314pp; English.
XX
CC The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial

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CC restenosis, rheumatoid arthritis, angina, myocardial infarctions.
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 666 AA;

Query Match          98.8%; Score 1048; DB 6; Length 666;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQPAGNQTSPGATEDYSYGSWYIDPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
DB 3 SQPAGNQTSPGATEDYSYGSWYIDPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VILLLLAMLVRRRLQWPCVGRGRLPSVDFLAGDRPRAVPAAVFMVLLSSCLLLPDED 121
DB 63 VILLLLAMLVRRRLQWPCVGRGRLPSVDFLAGDRPRAVPAAVFMVLLSSCLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLIGSTLSWA 181
DB 123 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLIGSTLSWA 182
QY 182 HLGQVQWQRAECQVPVKI 199
DB 183 HLGQVQWQRAECQVPVKI 200

RESULT 4
AAU04557
ID AAU04557 standard; protein; 667 AA.
AC
XX
XX AAU04557;
DT
XX 26-SEP-2001 (first entry)
XX
DE Human Stra6 homologue, PRO10282.
XX
KW Human; Stra6; PRO10282; 15q23; tumour; breast cancer; head tumour;
KW leukaemia; lymphoid malignancy; inflammatory disorder;
KW immunogenic disorder; antigen; antibody.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 8..12
FT /note= "Asn is N-glycosylated"
FT Region 50..56
FT Domain 54..69
FT /label= N_myristoylation_site
FT Region 89..97
FT /label= Transmembrane_domain
FT /note= "Region deleted in Stra6 variant PRO19578"
FT Domain 102..119
FT /label= Transmembrane_domain
FT Region 132..140
FT /note= "ATP/GTP-binding site motif A (P-loop)"
FT Domain 148..166
FT /label= Transmembrane_domain
FT Region 176..182
FT /label= N_myristoylation_site
FT Domain 207..222
FT /label= Transmembrane_domain
FT Region 241..247
FT /label= N_myristoylation_site
FT Domain 301..320
FT /label= Transmembrane_domain
FT Region 317..323
FT /label= N_myristoylation_site
FT Region 341..347
FT /label= N_myristoylation_site
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FT Domain 364..380
FT /label= Transmembrane_domain
FT Region 364..375
FT /note= "Prokaryotic membrane lipoprotein attachment site"
FT Domain 431..451
FT /label= Transmembrane_domain
FT Domain 474..489
FT /label= Transmembrane_domain
FT Region 525..531
FT /label= N_myristoylation_site
FT Domain 560..535
FT /label= Transmembrane_domain
FT Region 627..633
FT /label= N_myristoylation_site
FT Region 631..637
FT /label= N_myristoylation_site
FT Region 640..646
FT /label= N_myristoylation_site
FT Region 661..667
FT /label= N_myristoylation_site
XX
XX WO200151635-A2.
XX
XX 19-JUL-2001.
XX
XX 11-JAN-2001; 2001WO-US000847.
XX
XX 13-JAN-2000; 2000US-0175849P.
XX 14-APR-2000; 2000US-0197089P.
XX 29-AUG-2000; 2000US-0228914P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Pennica D, Smith V, Wood WI;
XX
XX WPI; 2001-442146/47.
XX N-PSDB; AAS08630.
XX
XX Human nucleic acid encoding a PRO10282 or PRO19578 polypeptide (the PRO
XX polypeptides are referred to as Stra6 polypeptides), useful in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping.
XX
XX Claim 24; Fig 2; 159pp; English.
XX
XX The sequence is human PRO10282, a homologue of murine Stra6, a retinoic
XX acid responsive protein thought to play an important role in early
XX dorsoventral limb patterning during development and later in the control
XX of endochondral ossification. The gene for the Stra6 homologue is located
XX on chromosome 15q23. The Stra6 polypeptides, agonists, antagonists or
XX anti-Stra6 antibodies are useful for preparation of a medicament useful
XX in the treatment of a condition which is responsive to the Stra6
XX polypeptides, agonists, antagonists or anti-Stra6 antibodies. The Stra6
XX polypeptides may also be employed as molecular weight markers for protein
XX electrophoresis. The Stra6 nucleic acids have applications in molecular
XX biology, including use as hybridisation probes, and in chromosome and
XX gene mapping. The antibodies and other anti-tumour compounds may be used
XX to treat various conditions, including those characterised by
XX overexpression and/or activation of amplified genes. Exemplary conditions
XX or disorders include benign or malignant tumours (e.g., renal, liver,
XX kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
XX pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
XX glioblastomas, and various head and neck tumours, leukaemias and lymphoid
XX malignancies), neuronal, glial, astrocytal, hypothalamic and other
XX glandular, macrophagal, epithelial, stromal and blastocoelec disorders,
XX inflammatory, angiogenic and immunogenic disorders
XX
XX SQ Sequence 667 AA;
```

Query Match 98.8%; Score 1048; DB 4; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASLSIL 61
 DB |||||
 QY 3 SOPAGNOTSPGATEDSYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASLSIL 62
 DB |||||
 QY 62 VLLLLAMLVRRRQLWPCVCRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
 DB |||||
 QY 63 VLLLLAMLVRRRQLWPCVCRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
 DB |||||
 QY 122 ALPFTLTASAPSDQKTEAPRGAWKILGLFYHAAALYPLAACATAGHTAAHLLGSTLSWA 181
 DB |||||
 QY 123 ALPFTLTASAPSDQKTEAPRGAWKILGLFYHAAALYPLAACATAGHTAAHLLGSTLSWA 182
 DB |||||
 QY 182 HLGQVQWQRAECPOVPKI 199
 DB |||||
 QY 183 HLGQVQWQRAECPOVPKI 200
 DB |||||

RESULT 5
 AAB88572
 ID AAB88572 standard; protein; 667 AA.
 XX
 AC AAB88572;
 DT
 DT 04-JUN-2001 (first entry)
 XX
 DE Human hydrophobic domain containing protein clone HP10713 #36.
 XX
 KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
 KW antianemic; vulnery; antiulcer; osteopathic; anti-inflammatory;
 KW cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
 KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
 KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
 KW behavioural characteristic; immune response.
 XX
 OS Homo sapiens.
 XX
 PN WO200112660-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 10-AUG-2000; 2000WO-JP005356.
 XX
 PR 17-AUG-1999; 99JP-00230344.
 PR 07-SEP-1999; 99JP-00252551.
 PR 01-OCT-1999; 99JP-00281132.
 PR 22-OCT-1999; 99JP-00301624.
 PR 04-NOV-1999; 99JP-00313877.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR WPI; 2001-160059/16.
 DR N-PSDB; AAF94442.
 XX
 PT Human proteins with hydrophobic domains and the DNAs which encode them
 PT are useful for treating autoimmune disorders, burns and tumors and for
 PT screening novel pharmaceuticals.
 XX
 PS Claim 1; Page 288-291; 518pp; English.
 PS
 XX AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
 CC AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
 CC anti-HIV, neuroprotective, antianemic, vulnery, antiulcer,
 CC osteopathic, anti-inflammatory and cytostatic activities, and can be used
 CC in gene therapy. (I) can be used as pharmaceuticals and as antigens to
 CC prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
 CC for genetic diagnosis and gene sources for gene therapy or for producing
 CC (I) in large quantities. Cells containing (II) are used for the detection
 CC of ligands or receptors corresponding to membrane or secretory proteins
 CC and to screen small molecule novel pharmaceuticals. Antibodies directed
 CC to (I) can be used for the detection, quantification and purification of

CC (I). Activities of (I) may include cytokine and cell
 CC proliferation/differentiation function, immune stimulating or suppressing
 CC activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
 CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.
 CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
 CC inflammatory bowel disease and tumours. (I) and (II) can also be used for
 CC wound healing, as nutritional sources or supplements e.g. as amino acid,
 CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
 CC processing and utilisation of dietary fat, protein, carbohydrate, to affect
 CC vitamins and minerals, to effect behavioural characteristics, to affect
 CC appetite, and can act as antigens in vaccines to raise an immune response
 CC to the protein or another material cross-reactive with the protein

XX Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 4; Length 667;
 Best Local Similarity 99.0%; Pred. No. 1.3e-105;
 Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASLSIL 61
 DB |||||
 QY 3 SOPAGNOTSPGATEDSYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASLSIL 62
 DB |||||
 QY 62 VLLLLAMLVRRRQLWPCVCRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
 DB |||||
 QY 63 VLLLLAMLVRRRQLWPCVCRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
 DB |||||
 QY 122 ALPFTLTASAPSDQKTEAPRGAWKILGLFYHAAALYPLAACATAGHTAAHLLGSTLSWA 181
 DB |||||
 QY 123 ALPFTLTASAPSDQKTEAPRGAWKILGLFYHAAALYPLAACATAGHTAAHLLGSTLSWA 182
 DB |||||
 QY 182 HLGQVQWQRAECPOVPKI 199
 DB |||||
 QY 183 HLGQVQWQRAECPOVPKI 200
 DB |||||

RESULT 6

AAU83631
 ID AAU83631 standard; protein; 667 AA.

XX
 AC AAU83631;
 DT
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 80.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.

XX Homo sapiens.

XX WO200208288-A2.

XX 31-JAN-2002.

XX 29-JUN-2001; 2001WO-US021066.

XX 20-JUL-2000; 2000US-0219556P.

XX 25-JUL-2000; 2000US-0220585P.

XX 25-JUL-2000; 2000US-0220605P.

XX 25-JUL-2000; 2000US-0220607P.

XX 25-JUL-2000; 2000US-0220624P.

XX 25-JUL-2000; 2000US-0220638P.

XX 25-JUL-2000; 2000US-0220666P.

XX 26-JUL-2000; 2000US-0220893P.

XX 28-JUL-2000; 2000WO-US020710.

XX 01-AUG-2000; 2000US-0222425P.

XX 22-AUG-2000; 2000US-0227133P.

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PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
DR N-PSDB; ABK33575.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
XX Claim 11; Fig 80; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
XX Sequence 667 AA;
XX
XX Query Match 98.8%; Score 1048; DB 5; Length 667;
XX Best Local Similarity 99.0%; Pred. No. 1.3e-105;
XX Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 2 SQPAGNQTSPGATEDYSGWYIDEPQGXELQPEGEVPSCHTSIPPLGYHACLASLSIL 61
DB 3 SQPAGNQTSPGATEDYSGWYIDEPQGXELQPEGEVPSCHTSIPPLGYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVGRGRLPSVDFLAGDRPRAVPAAVFMVLLSLCLLLPDED 121
DB 63 VLLLLAMLVRRRLQWPCVGRGRLPSVDFLAGDRPRAVPAAVFMVLLSLCLLLPDED 122
QY 122 ALPFLTLASAPSQGKTEAPRGANKILGLFYAALYVPLAACATAGTAHAHLGSLTSLWA 181
DB 123 ALPFLTLASAPSQGKTEAPRGANKILGLFYAALYVPLAACATAGTAHAHLGSLTSLWA 182
QY 182 HLGQVWQWQARCPQVPKI 199
DB 183 HLGQVWQWQARCPQVPKI 200
XX
XX RESULT 7
XX AAU78575
XX ID AAU78575 standard; protein; 667 AA.
XX
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AC AAU78575;
XX 18-JUN-2002 (first entry)
XX
DE Human Stra6 (PRO10282) protein.
XX
KW Human; cancer; Stra6; PRO10282; cytotatic; stromal disorder; tumour;
KW retinoid; Wnt; tumour antigen; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; blastocoeic disorder; chromosome 15q23.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 8..12
XX /note= "N Glycosylation site"
XX Region 50..56
XX /note= "N-myristoylation site"
XX Domain 54..69
XX /note= "Transmembrane domain"
XX Domain 102..119
XX /note= "Transmembrane domain"
XX Region 132..140
XX /note= "ATP/GTP binding site motif A"
XX Domain 148..166
XX /note= "Transmembrane domain"
XX Region 176..182
XX /note= "N-myristoylation site"
XX Domain 207..222
XX /note= "Transmembrane domain"
XX Region 241..247
XX /note= "N-myristoylation site"
XX Domain 301..320
XX /note= "Transmembrane domain"
XX Region 317..323
XX /note= "N-myristoylation site"
XX Region 341..347
XX /note= "N-myristoylation site"
XX Domain 364..380
XX /note= "Transmembrane domain"
XX Region 364..375
XX /note= "lipoprotein lipid attachment site"
XX Domain 431..451
XX /note= "Transmembrane domain"
XX Domain 474..489
XX /note= "Transmembrane domain"
XX Region 525..531
XX /note= "N-myristoylation site"
XX Domain 560..535
XX /note= "Transmembrane domain"
XX Region 627..633
XX /note= "N-myristoylation site"
XX Region 631..637
XX /note= "N-myristoylation site"
XX Region 640..646
XX /note= "N-myristoylation site"
XX Region 661..667
XX /note= "N-myristoylation site"
XX
XX WO200218608-A2.
XX
XX 07-MAR-2002.
XX
XX 10-JUL-2001; 2001WO-US021635.
XX
XX 29-AUG-2000; 2000US-0228914P.
XX 11-JAN-2001; 2001US-00759056.
XX 10-JUL-2001; 2001US-00901812.
XX
XX (GETH ) GENENTECH INC.
XX
XX Tice D, Pennica D, Polakis P, Szeto W;
XX
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XX WPI: 2002-292202/33.
 DR N-PSDB; ABK47278.
 XX
 PT Selectively enhancing the expression of a protein in a tumor cell
 PT characterized by aberrant Wnt signaling, useful for enhancing the
 PT efficacy of treatment of cancers, comprises treating the tumor cell with
 XX a retinoid.
 PS Example 1; Fig 2; 141pp; English.
 XX
 CC This invention relates to a novel method for selective enhancement of the
 CC expression of a protein in a tumor cell characterized by aberrant Wnt
 CC signaling by treating the tumor cell with a retinoid. The method is
 CC useful for enhancing the efficacy of treatment of cancers characterized
 CC by aberrant Wnt signaling, and for identifying tumor antigens the
 CC expression of which is selectively enhanced by retinoid treatment. The
 CC method is also useful in the early detection of tumors for early
 CC intervention. The tumor antigens are useful as targets for cancer
 CC therapy, since selective enhancement of their expression by retinoid
 CC treatment relative to normal cells improves the efficacy and therapeutic
 CC index of cancer therapeutics directed against these antigens. Antibodies
 CC binding to the tumor antigens may be administered for the treatment of
 CC various disorders or conditions, including those characterized by
 CC overexpression and/or activation of the tumor antigens, where such
 CC conditions or disorders include benign or malignant tumors; leukaemias
 CC and lymphoid malignancies; neuronal, glial, astrocytal, hypothalamic and
 CC other glandular, macrophagal, epithelial, stromal and blastocoeleic
 CC disorders. The present sequence represents the human Stra6 protein
 CC (PRO10282) which is selectively upregulated by retinoid using the method
 CC of the invention. The gene encoding the human Stra6 protein is located on
 CC human chromosome 15q23
 XX
 SQ Sequence 667 AA;
 Query Match 98.8%; Score 1048; DB 5; Length 667;
 Best Local Similarity 99.0%; Pred. No. 1.3e-105;
 Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 SQPAGNQTSPGATEDSYSGSWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
 Db 3 SQPAGNQTSPGATEDSYSGSWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
 QY 62 VLLLLAMLVRRRLQWPCVRCRPGPLSPVDFLAGDRPRAPVPAVFWVLLSSICLLLPDBD 121
 Db 63 VLLLLAMLVRRRLQWPCVRCRPGPLSPVDFLAGDRPRAPVPAVFWVLLSSICLLLPDBD 122
 QY 122 ALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLLGSTLSWA 181
 Db 123 ALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLLGSTLSWA 182
 QY 182 HLGQVQWQRAECQPVPKI 199
 Db 183 HLGQVQWQRAECQPVPKI 200
 RESULT 9
 AAO19413
 ID AAO19413 standard; protein; 667 AA.
 XX AAO19413;
 AC
 XX 10-DEC-2002 (first entry)
 DT
 XX Human molecule for disease detection and treatment protein #16.
 DE
 XX Human; molecule for disease detection and treatment; MDDT; gene therapy;
 KW cystostatic; antiarteriosclerotic; hepatotropic; anti-HIV; antiallergic;
 KW antiinflammatory; antiaerthmatic; cerebroprotective; nootropic;
 KW neuroprotective; antiparkinsonian; cardiant; antianginal.
 XX
 OS Homo sapiens.
 XX

PN WO200270709-A2.
 XX
 PD 12-SEP-2002.
 XX
 PF 08-FEB-2002; 2002MO-US003709.
 XX
 PR 09-FEB-2001; 2001US-0268117P.
 PR 15-FEB-2001; 2001US-0269618P.
 PR 23-FEB-2001; 2001US-0271118P.
 PR 07-MAR-2001; 2001US-0274486P.
 PR 09-MAR-2001; 2001US-0274436P.
 PR 28-NOV-2001; 2001US-0334229P.
 PR 01-FEB-2002; 2002US-0353284P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal PG, Baughn MR, Yao MG, Wallia NK, Elliot VS, Xu Y;
 PI Honchell CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DAM;
 PI Hafalia AJA, Ghandi AR, Thangavelu K, Sanjanwala MM, Tang YT;
 PI Ramkumar J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein SK;
 PI Burford N, Lee EA, Lu Y, Tran UK, Marquis JP;
 XX
 DR WPI; 2002-713453/77.
 XX N-PSDB; AAL49942.
 DR
 CC New human molecules for disease detection and treatment (MDDT), useful
 CC for diagnosing, treating and preventing diseases or conditions associated
 CC with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
 CC hepatitis.
 XX
 PS Claim 1; Page 148-150; 177pp; English.
 XX
 CC The present invention relates to human proteins and coding sequences of
 CC molecules for disease detection and treatment MDDT. The sequences can be
 CC used in the treatment of diseases associated with the decreased
 CC expression or overexpression of MDDT, such as cell proliferative (cancer,
 CC atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS,
 CC allergies, Addison's disease, asthma), developmental (dwarfism, renal
 CC tubular acidosis), neurological (e.g. stroke, Parkinson's disease,
 CC epilepsy) and cardiovascular (congestive heart failure, myocardial
 CC infarction, angina pectoris) disorders. The present sequence is a protein
 CC of the invention
 XX
 SQ Sequence 667 AA;
 Query Match 98.8%; Score 1048; DB 5; Length 667;
 Best Local Similarity 99.0%; Pred. No. 1.3e-105;
 Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 SQPAGNQTSPGATEDSYSGSWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
 Db 3 SQPAGNQTSPGATEDSYSGSWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
 QY 62 VLLLLAMLVRRRLQWPCVRCRPGPLSPVDFLAGDRPRAPVPAVFWVLLSSICLLLPDBD 121
 Db 63 VLLLLAMLVRRRLQWPCVRCRPGPLSPVDFLAGDRPRAPVPAVFWVLLSSICLLLPDBD 122
 QY 122 ALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLLGSTLSWA 181
 Db 123 ALPFLTLASAPSDGKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLLGSTLSWA 182
 QY 182 HLGQVQWQRAECQPVPKI 199
 Db 183 HLGQVQWQRAECQPVPKI 200
 RESULT 9
 ADA54816
 ID ADA54816 standard; protein; 667 AA.
 XX ADA54816;
 AC
 XX 20-NOV-2003 (first entry)
 DT

XX DE Human protein, SEQ ID 2384.
XX KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX KW Homo sapiens.
OS EP1293569-A2.
XX PN 19-MAR-2003.
XX PD 21-MAR-2002; 2002EP-00006586.
XX PP 14-SEP-2001; 2001JP-00328381.
XX PR 24-JAN-2002; 2002US-0350435P.
XX PA (HELI-) HELIX RES INST.
XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-395539/38.
DR N-PSDB; ADA53177.
XX XX
XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX PS Claim 14; SEQ ID NO 2384; 205pp; English.
XX XX
XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX XX
SQ Sequence 667 AA;
Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SQPAGNQTSPGATEDYSGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
DB 3 SQPAGNQTSPGATEDYSGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVGRGRLPSVDPLAGDRPRAVPAVFMVLLSSCLLLPDED 121
DB 63 VLLLLAMLVRRRLQWPCVGRGRLPSVDPLAGDRPRAVPAVFMVLLSSCLLLPDED 122
QY 122 ALPFLTILASAPSDGKTEAPRGAWKILGLFYAALYPLAACATAGTAHLLGSLTSLWA 181
DB 123 ALPFLTILASAPSDGKTEAPRGAWKILGLFYAALYPLAACATAGTAHLLGSLTSLWA 182
QY 182 HLGQVWQRAECPOVPKI 199
DB 183 HLGQVWQRAECPOVPKI 200
RESULT 10
ABU80778
ID ABU80778 standard; protein; 667 AA.
XX AC ABU80778;
XX XX
DT 23-JUN-2003 (first entry)
XX XX
DE Human PRO polypeptide #40.
XX XX

KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX OS Homo sapiens.
XX PN US2003036635-A1.
XX PD 20-FEB-2003.
XX PF 28-AUG-2002; 2002US-00230163.
XX PR 25-JUL-2000; 2000US-0220638P.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021065.
XX PR 09-APR-2002; 2002US-00119480.
XX XX
XX (GETH) GENENTECH INC.
XX XX
XX Baker KP, Deenoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
XX N-PSDB; ACA66880.
XX DR One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX PT useful for the manufacture of a medicament for diagnosing or treating
XX PT tumor.
XX PS Claim 11; Fig 80; 314pp; English.
XX XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/paipsIDEntry.html
XX XX
SQ Sequence 667 AA;
Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SQPAGNQTSPGATEDYSGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
DB 3 SQPAGNQTSPGATEDYSGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVGRGRLPSVDPLAGDRPRAVPAVFMVLLSSCLLLPDED 121
DB 63 VLLLLAMLVRRRLQWPCVGRGRLPSVDPLAGDRPRAVPAVFMVLLSSCLLLPDED 122
QY 122 ALPFLTILASAPSDGKTEAPRGAWKILGLFYAALYPLAACATAGTAHLLGSLTSLWA 181
DB 123 ALPFLTILASAPSDGKTEAPRGAWKILGLFYAALYPLAACATAGTAHLLGSLTSLWA 182
QY 182 HLGQVWQRAECPOVPKI 199
DB 183 HLGQVWQRAECPOVPKI 200
RESULT 11
ABO33744
ID ABO33744 standard; protein; 667 AA.
XX AC ABO33744;
XX XX
DT 17-SEP-2003 (first entry)
XX XX

```

DE XX Novel human secreted and transmembrane protein PRO10282.
KW XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW XX antarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW XX chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW XX pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW XX colon tumour; breast tumour; prostate tumour; rectal tumour;
KW XX liver tumour; bone disorder; cartilage disorder; sports injury;
KW XX arthritis; wound.
XX OS Homo sapiens.
XX PN US2003045687-A1.
XX PD 06-MAR-2003.
XX PF 12-AUG-2002; 2002US-00218631.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX XX WPI; 2003-512315/48.
XX DR N-PSDB; ACD68632.
XX XX New genes, and its encoded secreted and transmembrane polypeptides,
XX PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
XX PT pericyte proliferation, especially for treating lung tumors, arthritis or
XX PT wounds in a mammal.
XX PS Claim 11; Fig 80; 314pp; English.
XX CC The invention describes an isolated nucleic acid molecule comprising a
XX CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
XX CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
XX CC fully defined in the specification; or (b) any of 122 nucleotide
XX CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
XX CC specification; or the full length coding sequence of any these 122
XX CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
XX CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
XX CC particularly useful for detecting tumours (e.g. lung tumour, colon
XX CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
XX CC in a mammal, for stimulating the release of TNF-alpha from human blood,
XX CC for stimulating the proliferation or differentiation of chondrocyte
XX CC cells, for stimulating proliferation of pericyte cells, or for modulating
XX CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
XX CC polypeptide is also useful for treating tumours or various bone and/or
XX CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
XX CC PRO polypeptides are useful in drug screening, particularly as targets
XX CC for therapeutic intervention in these diseases, and in the diagnostic
XX CC determination of the presence of these diseases. The PRO polypeptides are
XX CC also useful as molecular weight markers, or for chromosome
XX CC identification. The PRO genes are useful as hybridisation probes, or for
XX CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
XX CC also be used in gene therapy, particularly for replacing a defective
XX CC gene. This is the amino acid sequence of a novel human secreted and
XX CC transmembrane PRO polypeptide
XX SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDYSYGSWIDEPQGGXELQPEGEVPSCHTSPPGLYHACLASLSL 61
Db 3 SOPAGNOTSPGATEDYSYGSWIDEPQGGXELQPEGEVPSCHTSPPGLYHACLASLSL 62

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QY 62 VLLLLAMLVRRRLQPLWPCVCRGPGLPSPVDFLAGDRPRAVPAAPVFWLLSSLCLLLPD 121
Db 63 VLLLLAMLVRRRLQPLWPCVCRGPGLPSPVDFLAGDRPRAVPAAPVFWLLSSLCLLLPD 122
QY 122 ALPFLTLASAPSDQDKTEAPRGAMKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
Db 123 ALPFLTLASAPSDQDKTEAPRGAMKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 182
QY 182 HLGQVQWQORACPQVPKI 199
Db 183 HLGQVQWQORACPQVPKI 200

RESULT 12
ABJ72267
ID ABJ72267 standard; protein; 667 AA.
XX AC ABJ72267;
XX DT 06-NOV-2003 (first entry)
XX DE Human PRO10282 protein.
XX KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
XX KW differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN US2003050448-A1.
XX PD 13-MAR-2003.
XX PF 28-AUG-2002; 2002US-00230414.
XX PR 01-JUN-2001; 2001WO-US017800.
XX PR 29-JUN-2001; 2001WO-US021066.
XX PR 09-APR-2002; 2002US-00119480.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX XX WPI; 2003-521818/49.
XX DR N-PSDB; ABT44265.
XX PT New nucleic acid encoding for a PRO protein, useful for the manufacture
XX PT of a medicament for diagnosing or treating tumors or for measuring or
XX PT detecting expression of an associated gene.
XX PS Claim 11; Fig 80; 315pp; English.
XX CC The invention relates to a novel isolated nucleic acid encoding a fully
XX CC defined PRO polypeptide. The molecules of the invention may be useful for
XX CC stimulating proliferation or gene expression in pericyte cells or the
XX CC release of TNF-alpha from human blood. Other possible uses include the
XX CC stimulation or inhibition of chondrocyte proliferation or
XX CC differentiation, the stimulation of human dermal fibroblast cell
XX CC proliferation and the detection of the presence of a tumour within a
XX CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
XX CC of a medicament for diagnosing or treating a tumour within a mammal or
XX CC for measuring or detecting the expression of an associated gene, as well
XX CC as during gene therapy. The current sequence is that of the human PRO
XX CC protein of the invention
XX SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDYSYGSWIDEPQGGXELQPEGEVPSCHTSPPGLYHACLASLSL 61

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Db 3 SQPAGNOTSPGATEDSYSGSWYIDEPQGGELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
Qy 62 VLLLLAMLVRRRLQPLWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
Db 63 VLLLLAMLVRRRLQPLWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
Qy 122 ALPFLTLASAPSDQSGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
Db 123 ALPFLTLASAPSDQSGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 182
Qy 182 HLGQVQWQRAECPQVPKI 199
Db 183 HLGQVQWQRAECPQVPKI 200

RESULT 13
ABJ72395
ID ABO34295 standard; protein; 667 AA.
XX
AC ABJ72395;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10282 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
OS Homo sapiens.
XX
XN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
PF 26-AUG-2002; 2002US-00227884.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-503301/47.
XX N-PSDB; ABT44548.
XX
XX New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
XX Claim 11; Fig 80; 324pp; English.

XX The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
XX Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SQPAGNOTSPGATEDSYSGSWYIDEPQGGELQPEGEVPSCHTSIPPGLYHACLASLSIL 61

Db 3 SQPAGNOTSPGATEDSYSGSWYIDEPQGGELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
Qy 62 VLLLLAMLVRRRLQPLWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
Db 63 VLLLLAMLVRRRLQPLWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
Qy 122 ALPFLTLASAPSDQSGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
Db 123 ALPFLTLASAPSDQSGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 182
Qy 182 HLGQVQWQRAECPQVPKI 199
Db 183 HLGQVQWQRAECPQVPKI 200

RESULT 14
ABO34290
ID ABO34290 standard; protein; 667 AA.
XX
AC ABO34290;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 10282.
XX
KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.
XX
OS Homo sapiens.
XX
XN US2003044934-A1.
XX
PD 06-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230338.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-492274/46.
XX N-PSDB; ACD82215.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
XX Claim 19; Fig 80; 315pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. Nucleic acids that encode PRO can be used to generate either
CC transgenic animals or knock-out animals useful in developing and
CC screening of therapeutically useful reagents. The nucleic acids may also
CC be used in gene therapy for replacing defective gene, in chromosome
CC identification, as chromosome markers, or in generating probes to isolate
CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
CC stimulation. TNF-alpha stimulation, human dermal fibroblasts stimulation
CC and for detecting the presence of tumour in an mammal. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
CC of a human secreted/transmembrane PRO polypeptide
XX

SQ Sequence 667 AA;
Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SOPAGNOTSPGATEDSYSGWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
DB 3 SOPAGNOTSPGATEDSYSGWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSICLLLPDED 121
DB 63 VLLLLAMLVRRRLQWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSICLLLPDED 122
QY 122 ALPFTLLASAPSDQKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
DB 123 ALPFTLLASAPSDQKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLGSLTSLWA 182
QY 182 HLGQVQWQRAECPQVPKI 199
DB 183 HLGQVQWQRAECPQVPKI 200
RESULT 15
ABJ72097
ID ABJ72097 standard; protein; 667 AA.
XX
AC ABJ72097;
XX
XX
DT 16-OCT-2003 (first entry)
XX
DE Human membrane bound receptor/protein PRO10282 amino acid sequence.
XX
KW Human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
XX US2003065147-A1.
XX
XX 03-APR-2003.
XX
XX 29-AUG-2002; 2002US-00232224.
XX
XX 28-JUL-1999; 99US-0146222P.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-522018/49.
DR N-PSDB; ABT43921.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 80; 315pp; English.
XX
XX This invention relates to one hundred and twenty two novel nucleic acids
XX encoding human PRO membrane bound proteins or receptors. Extracellular
XX proteins play important roles in the formation, differentiation and
XX maintenance of multicellular organisms. The fate of many individual cells
XX (for example proliferation, migration or differentiation) is typically

CC governed by information received from other cells and the immediate
CC environment. The information is often transmitted by secreted
CC polypeptides (for example mitogenic factors, survival factors, cytotoxic
CC factors, differentiation factors, neurotrophic factors and hormones) which are
CC received and interpreted by diverse cell receptors or membrane bound
CC proteins. These membrane bound proteins and receptors may be of use as
CC pharmaceutical and diagnostic agents, such as in the blocking of receptor
CC -ligand interactions. The current invention provides the amino acid
CC sequences of novel human membrane bound receptors and proteins, along
CC with the cDNA sequences encoding them. The novel proteins of the
CC invention may have cytostatic activities through the stimulation of
CC chondrocytes. The nucleic acids of the invention may be useful for the
CC manufacture of a medicament for diagnosing or treating a tumour in a
CC mammal. In addition, they may be useful for measuring or detecting the
CC expression of a tumour associated gene. The present sequence is the amino
CC acid sequence of a human PRO protein of the invention
XX
SQ Sequence 667 AA;
Query Match 98.8%; Score 1048; DB 7; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SOPAGNOTSPGATEDSYSGWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
DB 3 SOPAGNOTSPGATEDSYSGWYIDBPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSICLLLPDED 121
DB 63 VLLLLAMLVRRRLQWPCVGRGPGLPSPVDFLAGDRPRAVPAAVFMVLLSSICLLLPDED 122
QY 122 ALPFTLLASAPSDQKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
DB 123 ALPFTLLASAPSDQKTEAPRGAWKILGLFYAALYYPPLAACATAGHTAAHLGSLTSLWA 182
QY 182 HLGQVQWQRAECPQVPKI 199
DB 183 HLGQVQWQRAECPQVPKI 200
Search completed: February 8, 2005, 13:36:11
Job time : 91.4866 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:30:00 ; Search time 23.5458 seconds
(without alignments)
630.905 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPNQTSPTGATEDSYGV.....WAHLGVQVWQRAECQVPEKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	8.3	509	4	US-09-252-991A-21709
2	85.5	8.1	380	3	US-08-924-345-2
3	84	7.9	913	4	US-09-140-378A-2
4	84	7.9	919	1	US-08-336-343A-2
5	84	7.9	937	4	US-09-949-016-8366
6	84	7.9	937	4	US-09-949-016-8367
7	84	7.9	937	4	US-09-949-016-8368
8	83	7.8	913	1	US-08-445-640-4
9	83	7.8	913	3	US-08-170-558-4
10	83	7.8	913	3	US-08-447-314-4
11	83	7.8	913	3	US-08-445-461-4
12	83	7.8	913	4	US-09-223-490-4
13	81	7.6	429	4	US-09-252-991A-30376
14	80.5	7.6	463	4	US-09-252-991A-19381
15	80	7.5	433	3	US-09-106-075A-86
16	80	7.5	699	5	PCT-US94-07297-39
17	80	7.5	921	1	US-08-336-479B-2
18	80	7.5	921	1	US-08-818-823-2
19	80	7.5	1171	4	US-09-417-197-131
20	80	7.5	1181	4	US-09-417-197-133
21	79.5	7.5	435	4	US-09-902-540-14931
22	79	7.4	505	1	US-08-221-750A-5
23	78.5	7.4	369	4	US-09-902-540-10817
24	78.5	7.4	532	4	US-09-949-016-6607
25	78.5	7.4	540	4	US-09-252-991A-22555
26	78.5	7.4	3519	3	US-09-428-517-4
27	78	7.4	475	4	US-09-252-991A-25837

28	77.5	7.3	535	4	US-09-949-016-10290	Sequence 10290, A
29	76.5	7.2	875	1	US-08-785-241-5	Sequence 5, Appli
30	76	7.2	478	4	US-09-902-540-10474	Sequence 10474, A
31	75	7.1	331	2	US-08-986-217-7	Sequence 7, Appli
32	75	7.1	575	4	US-09-949-016-9760	Sequence 9760, Ap
33	74.5	7.0	337	4	US-09-252-991A-23066	Sequence 23066, A
34	74.5	7.0	482	4	US-09-252-991A-23559	Sequence 23559, A
35	74.5	7.0	657	4	US-09-902-540-12047	Sequence 12047, A
36	73.5	6.9	147	4	US-09-252-991A-29490	Sequence 29490, A
37	73.5	6.9	311	4	US-09-252-991A-30973	Sequence 30973, A
38	73.5	6.9	356	4	US-09-602-777A-424	Sequence 424, App
39	73.5	6.9	378	3	US-09-482-180A-2	Sequence 2, Appli
40	73.5	6.9	578	1	US-08-653-740-3	Sequence 3, Appli
41	73.5	6.9	578	3	US-09-073-594-3	Sequence 3, Appli
42	73.5	6.9	578	3	US-09-275-925-3	Sequence 3, Appli
43	73.5	6.9	636	1	US-08-653-740-5	Sequence 5, Appli
44	73.5	6.9	636	2	US-09-073-594-5	Sequence 5, Appli
45	73.5	6.9	636	3	US-09-275-925-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-21709
; Sequence 21709, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21709
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-21709

Query Match	8.3%	Score 88;	DB 4;	Length 509;
Best Local Similarity	27.3%	Pred. No. 0.3;		
Matches	51;	Conservative 13;	Mismatches 65;	Indels 58; Gaps 12;
QY	26	EPQGXELQPEGEVPSCH-----TSIPPGLYHACLASLSILVLLMLVRRQLW----	76	
Db	188	EPQPGGLRAPGALPADHRGSRVPRDFPP---HA--AGLS-----NRRHGAWRSPA	232	
QY	77	---PDC--VRGRCLSPVDF-----LAGDRPRAPAAVFMVLLSLCLLLPDEDALPF	125	
Db	233	GATACRMLAGLPGGHGGLDHRVAGPAGGTTATRAPAA-----GTLCRAPPAALSR	287	
QY	126	LTLASA-----PSODGKTEAPRGAW-----KILGLFHYAALYYP-----LAACATAGH	168	
Db	288	RGVRAGVFPFRPRDAATLGQRGAGPVARSLLRRIPGAFQYQP-HYFSDPADLVPAANAAGR	346	
QY	169	TAHLLG 175		
Db	347	TQARTGG 353		

RESULT 2
US-08-924-345-2
; Sequence 2, Application US/08924345
; Patent No. 6224878
; GENERAL INFORMATION:
; APPLICANT: LEUNG-TACK Patricia
; APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree

```
; APPLICANT: AUDONNET Jean-Christophe, Francis
; APPLICANT: RIVIERE Michel, Emile, Albert
; TITLE OF INVENTION: Mutants and vaccines of the Infectious
; TITLE OF INVENTION: Mutants and vaccines of the Infectious
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LARSON AND TAYLOR
; STREET: 727 SOUTH TWENTY-THIRD STREET
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,345
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,172
; FILING DATE: 03-AUG-1994
; APPLICATION NUMBER: FR 92 07930
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SARRO, THOMAS P.
; REGISTRATION NUMBER: 19396
; REFERENCE/DOCKET NUMBER: XI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 920-7200
; TELEFAX: (703) 892-8428
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-924-345-2

Query Match 8.1%; Score 85.5; DB 3; Length 380;
Best Local Similarity 27.6%; Pred. No. 0.38; Indels 47; Gaps 6;
Matches 37; Conservative 12; Mismatches 38;

QY 4 PAGNOTSPGATEDYSGWYIDEPQGGXELQPEGEVPSCHTSIPPCLYHACLAS----LS 59
Db 256 PAGTASPAASPSRAFSA-----AAPAAAAQAGDTFA-----RFRQLASILVPLC 302
QY 60 ILVLLILLAM-----LVRRQI-----WPDGVRGRLGSPV 90
Db 303 VLVLALLALCAATVNCALRRLLPCSRVYKPTCAACSGTCAGRGPCRGAAPSAPATV 362
QY 91 DFLAGDRPRAVPA 104
Db 363 VAL-GSRPKAPPLA 375

RESULT 3
US-09-140-378A-2
; Sequence 2, Application US/09140378A
; Patent No. 6627733
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Rutter, William J.
; APPLICANT: Edman, Jeffrey C.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Receptor Tyrosine Kinase with a Discoidin-Type Binding
; TITLE OF INVENTION: Domain
; FILE REFERENCE: 023070-079010US
; CURRENT APPLICATION NUMBER: US/09/140,378A
; CURRENT FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 08/077,254
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; PRIOR FILING DATE: 1993-06-14
; PRIOR APPLICATION NUMBER: US 08/292,299
; PRIOR FILING DATE: 1994-08-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: discoidin domain receptor (DDR) tyrosine kinase
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(18)
; OTHER INFORMATION: signal peptide
; NAME/KEY: SITE
; LOCATION: (19)..(24)
; OTHER INFORMATION: uncertain point of signal peptide cleavage between amino acids 19
; NAME/KEY: DOMAIN
; LOCATION: (31)..(185)
; OTHER INFORMATION: discoidin I-type domain
; NAME/KEY: SITE
; LOCATION: (374)..(415)
; OTHER INFORMATION: proline/glycine-rich portion of connecting region interrupted by
; NAME/KEY: TRANSMEM
; LOCATION: (417)..(439)
; OTHER INFORMATION: transmembrane domain
; NAME/KEY: SITE
; LOCATION: (466)..(601)
; OTHER INFORMATION: proline/glycine-rich portion of connecting region interrupted by
; NAME/KEY: TURN
; LOCATION: (510)..(513)
; OTHER INFORMATION: tight turn recognition motif for internalization in coated pits
; NAME/KEY: DOMAIN
; LOCATION: (616)..(905)
; OTHER INFORMATION: tyrosine kinase domain
; US-09-140-378A-2

Query Match 7.9%; Score 84; DB 4; Length 913;
Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDYSGWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
Db 370 NNSPFGALGGTPPAPWPPGPPNFFSLELEPRGQQVAKAEGSPTAILGCLVAIILL 429
QY 62 VLLLLAMLV-----RRRLWPD-----CVRGRPGLPSPVDFL---- 93
Db 430 LLLIILMLWRLHWRLLSKAERVLEELTVHLVSGDITILINNRPGPREPPPYQEPRP 489
QY 94 AGDRPRAVPAAVFVLLSSCLLLPDELDALPFLTLASAPSODGKTEAPRGAW 145
Db 490 RGNPPHSAPC----VPNGSALLSNPARYRLLLATYARPPRGFG---PPTPAW 534

RESULT 4
US-08-336-343A-2
; Sequence 2, Application US/08336343A
; Patent No. 5677144
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Alves, Frauke
; TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,343A
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7693-065
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-336-343A-2

Query Match 7.9%; Score 84; DB 1; Length 919;
Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;
QY 7 NOTSPGATEDSYGSHWIDEPO-----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
DB 370 NNSSPALGGTFFPAPWPPPTNFSLEPRGQOPVAKAEGSTAILIGCLVAIILL 429
QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL----- 93
DB 430 LLLIALLMLRLHWRLLSKAERVLEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489
QY 94 AGDRPRAVPAAVFVWVLLSSCLLLPDEDALPFLTILASAPSDQKTEAPRGAW 145
DB 490 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 534

RESULT 5
US-09-949-016-8366
Sequence 8366, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8366
LENGTH: 937
TYPE: PRT
ORGANISM: Human
US-09-949-016-8366

Query Match 7.9%; Score 84; DB 4; Length 937;
Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;
QY 7 NOTSPGATEDSYGSHWIDEPO-----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
DB 394 NNSSPALGGTFFPAPWPPPTNFSLEPRGQOPVAKAEGSTAILIGCLVAIILL 453
QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL-----, 93

DB 454 LLLIALLMLRLHWRLLSKAERVLEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 513
QY 94 AGDRPRAVPAAVFVWVLLSSCLLLPDEDALPFLTILASAPSDQKTEAPRGAW 145
DB 514 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 558
RESULT 6
US-09-949-016-8367
Sequence 8367, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8367
LENGTH: 937
TYPE: PRT
ORGANISM: Human
US-09-949-016-8367
Query Match 7.9%; Score 84; DB 4; Length 937;
Best Local Similarity 22.7%; Pred. No. 1.9;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;
QY 7 NOTSPGATEDSYGSHWIDEPO-----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
DB 394 NNSSPALGGTFFPAPWPPPTNFSLEPRGQOPVAKAEGSTAILIGCLVAIILL 453
QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL----- 93
DB 454 LLLIALLMLRLHWRLLSKAERVLEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 513
QY 94 AGDRPRAVPAAVFVWVLLSSCLLLPDEDALPFLTILASAPSDQKTEAPRGAW 145
DB 514 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 558

RESULT 7
US-09-949-016-8368
Sequence 8368, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8368
LENGTH: 937
TYPE: PRT
ORGANISM: Human

US-09-949-016-8368

Query Match 7.9%; Score 84; DB 4; Length 937;

Best Local Similarity 22.7%; Pred. No. 1.9;

Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDSYSGWYIDEPQ----GGXELQPEGEVPSCHT-STIPPGLYHACLASLSTL 61

Db 394 NNSSPALGGTTPPAPWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILGCLVAIILL 453

QY 62 VILLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL----- 93

Db 454 LLLIIALMLRHLWRLLSKAERRVLEBELTVHLSVPGDTILNNRPGPREPPYQEP 513

QY 94 AGDRPRAVPAVFMVLLSSCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145

Db 514 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 558

RESULT 8

US-08-445-640-4

; Sequence 4, Application US/08445640

; Patent No. 5709858

; GENERAL INFORMATION:

; APPLICANT: Godowski, Paul J.

; APPLICANT: Mark, Melanie R.

; APPLICANT: Scadden, David T.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Baron, Will F.

; TITLE OF INVENTION: Protein Tyrosine Kinases

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/445,640

; FILING DATE: 22-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/170558

; FILING DATE: 20-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/157563

; FILING DATE: 23-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 854C2

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; TELEEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 913 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-445-640-4

Query Match

Best Local Similarity 22.7%; Pred. No. 2.4;

Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDSYSGWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSTL 61

Db 370 NNSSPALGGTTPPAPWPPGPPPTNFSSLELEPRGQQPVAKPEGSTAILGCLVAIILL 429

QY 62 VILLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL----- 93

Db 430 LLLIIALMLRHLWRLLSKAERRVLEBELTVHLSVPGDTILNNRPGPREPPYQEP 489

QY 94 AGDRPRAVPAVFMVLLSSCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145

Db 490 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 534

RESULT 9

US-08-170-558-4

; Sequence 4, Application US/08170558

; Patent No. 6001621

; GENERAL INFORMATION:

; APPLICANT: Godowski, Paul J.

; APPLICANT: Mark, Melanie R.

; APPLICANT: Scadden, David T.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Baron, Will F.

; TITLE OF INVENTION: Protein Tyrosine Kinases

; NUMBER OF SEQUENCES: 35

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/170,558

; FILING DATE: 20-DEC-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/157563

; FILING DATE: 23-NOV-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 854C1

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; TELEEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 913 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-170-558-4

Query Match 7.8%; Score 83; DB 3; Length 913;

Best Local Similarity 22.7%; Pred. No. 2.4;

Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDSYSGWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSTL 61

Db 370 NNSSPALGGTTPPAPWPPGPPPTNFSSLELEPRGQQPVAKPEGSTAILGCLVAIILL 429

QY 62 VILLAMLV-----RRQLWPD-----CVRGRGLPSPVDFL----- 93

Db 430 LLLIIALMLRHLWRLLSKAERRVLEBELTVHLSVPGDTILNNRPGPREPPYQEP 489

QY 94 AGDRPRAVPAVFMVLLSSCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145

Db 490 RGNPPHSAPC-----VPNGSALLSNPAYRLLLATYARPPRGPG---PPTPAW 534

RESULT 10
US-08-447-314-4
; Sequence 4, Application US/08447314
; Patent No. 6087144
; GENERAL INFORMATION:
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,461
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/170558
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/157563
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 854C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-445-461-4

Query Match 7.8%; Score 83; DB 3; Length 913;
Best Local Similarity 22.7%; Pred. No. 2.4;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDSYGWSYIDEPQ-----GGXELQPEGEVPSCH-TSIPPLGYHACLASLSIL 61
Db 370 NNSSPALGCTFPAPWPPGPPPTNFSLEPRGQOPVAKPEGSPATILIGCLVAIILL 429

QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRGLSPVDLFL----- 93
Db 430 LLLIIALLMRLHWRLLSKAERVLLEELTVHLSVPGDTILINNRPGPREPPYQPRP 489

QY 94 AGDRPRAVPAVFMVLLSSCLLLPDEDPALPFLTLASAPSDGKTEAPRGAW 145
Db 490 RGNPPHSAPC-----VPGNSALLSNPAYRLLLATYARPPRPGP---PPTPAW 534

RESULT 12
US-09-223-490-4
; Sequence 4, Application US/09223490
; Patent No. 6825324
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

US-08-447-314-4
; Sequence 4, Application US/08447314
; Patent No. 6087144
; GENERAL INFORMATION:
; APPLICANT: Scadden, David T.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Baron, Will F.
; TITLE OF INVENTION: Protein Tyrosine Kinases
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,314
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/170558
; FILING DATE: 20-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/157563
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 854C1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 913 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-447-314-4

Query Match 7.8%; Score 83; DB 3; Length 913;
Best Local Similarity 22.7%; Pred. No. 2.4;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSPGATEDSYGWSYIDEPQ-----GGXELQPEGEVPSCH-TSIPPLGYHACLASLSIL 61
Db 370 NNSSPALGCTFPAPWPPGPPPTNFSLEPRGQOPVAKPEGSPATILIGCLVAIILL 429

QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRGLSPVDLFL----- 93
Db 430 LLLIIALLMRLHWRLLSKAERVLLEELTVHLSVPGDTILINNRPGPREPPYQPRP 489

QY 94 AGDRPRAVPAVFMVLLSSCLLLPDEDPALPFLTLASAPSDGKTEAPRGAW 145
Db 490 RGNPPHSAPC-----VPGNSALLSNPAYRLLLATYARPPRPGP---PPTPAW 534

RESULT 11
US-08-445-461-4
; Sequence 4, Application US/08445461
; Patent No. 6096527
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.

STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/223,490
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/170,558
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hasak, Janet E.
 REGISTRATION NUMBER: 28,616
 REFERENCE/DOCKET NUMBER: 854C1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1896
 TELEFAX: 415/952-3881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 913 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-223-490-4

Query Match 7.8%; Score 83; DB 4; Length 913;

Best Local Similarity 22.7%; Pred. No. 2.4; Mismatches 20; Indels 40; Gaps 7;

Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;

QY 7 NOTSGATEDYSGWYIDEPQ---GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
 DB 370 NNSPAGLGTFPPAPWPPGPTNFFSSLELEPRGQPVAKPEGSPAILICLVAILL 429
 QY 62 VLLLLAMLV-----RRQLWPD-----CVRGRPLSPVDFL---- 93
 DB 430 LLLIITALLMLWRLHWRLLSKAERRVLEELTVHLSVPGDTILINNRPGPREPPYQEPRP 489
 QY 94 AGDRPRAVPAAVFVLLSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
 DB 490 RGNPHSAPC-----VNGSALLSNPAYKLLATYARPPRGG-----PPTPAW 534

RESULT 13
 US-09-252-991A-30376
 ; Sequence 30376, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 30376
 ; LENGTH: 429
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30376

Query Match 7.6%; Score 81; DB 4; Length 429;

Best Local Similarity 30.4%; Pred. No. 1.5;

Matches 56; Conservative 8; Mismatches 70; Indels 50; Gaps 9;

QY 33 LOPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRR---QLWPD-----CVRGRPG 85
 DB 83 LHPRHQPDHRHRRFPF--VRSQABRTIDGGHVRPVPVRRRTSLQLWPDREERGIRGKQ 140
 QY 86 LPSVDFLAGDRPRAVPAAVFVLLSLCLLLPDEDALP-----FLTLASAPSQDGKTE 139
 DB 141 -----LGGIQPAAGSA-----LPRQADHRQRRLGFL---SHPGQAGAPD 177
 QY 140 AP-----RGAWKILGLFHYAALYPLAACA---TAGHTAAHLGLSTLSWAHLGVQV 187
 DB 178 VPHLPAGGEAGRYPHPPGAFRPAALRQAPADPAPGRASGAAALLEGSRLLPRHLHRAA 237
 QY 188 WQRA 191
 DB 238 QQRS 241

RESULT 14

US-09-252-991A-19381
 ; Sequence 19381, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19381
 ; LENGTH: 463
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19381

Query Match 7.6%; Score 80.5; DB 4; Length 463;

Best Local Similarity 29.0%; Pred. No. 1.8;

Matches 54; Conservative 14; Mismatches 57; Indels 61; Gaps 13;

QY 27 PQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRRQLWPDVCRGP-- 84
 DB 226 PLGGQWLADLGGHP-----AVFATLAVLLASLAALV---PWPET---RPLL 267
 QY 85 -GLPSPVDF-----LAGDRP---RAVPAAVFVLLSLCL-----LILLPDEDALPF---LT 127
 DB 268 AGTPEPATLAIFFRVLRVLRPLQTRALLVAVLVNLFVSFYAAGPFVWGLPGLGFWIGLA 327
 QY 128 LASAPSDG--KTEAPRGAWKI-----LGLFHYAALYPLAACAAGTAHLLGST--- 177
 DB 328 IAIAGSLGALLNRRLLR--TWSARRVRLGL-----ALAAAGATAQTLLAAVGA 375
 QY 178 --LSWA 181
 DB 376 EGLYWA 381

RESULT 15

US-09-106-075A-86
 ; Sequence 86, Application US/09106075A
 ; Patent No. 6316250
 ; GENERAL INFORMATION:
 ; APPLICANT: Hjellev MD, Brian
 ; APPLICANT: Jenison, Steve
 ; TITLE OF INVENTION: Molecular Clones Producing Recombinant DNA Antigens of
 ; TITLE OF INVENTION: the HARDS Virus.
 ; FILE REFERENCE: 10312-801, Hjellev et al. (210312.0009)
 ; CURRENT APPLICATION NUMBER: US/09/106,075A

Tue Feb 8 14:19:16 2005

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; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 08/210,762
; PRIOR FILING DATE: 1994-03-22
; PRIOR APPLICATION NUMBER: 08/141,035
; PRIOR FILING DATE: 1993-10-26
; PRIOR APPLICATION NUMBER: 08/120,096
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/111,519
; PRIOR FILING DATE: 1993-08-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 86
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Prospect Hill virus
US-09-106-075A-86

Query Match      7.5%; Score 80; DB 3; Length 433;
Best Local Similarity 24.1%; Pred. No. 1.9;
Matches 35; Conservative 21; Mismatches 55; Indels 34; Gaps 6;

QY      23 YIDPQGGXELQPEGEVPSCHTSIPGLYHACLASLSILVLL-----LAMLYRRQLWPD 78
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      178 YVSMPTAQSTMKAELTPGRFTIVCGLEPAQIMARNIISPVMGIVGFAFFVKD---WAD 234
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      79 CVRG-----RGLPS-PVDFLAGDRPRAVPAAVFVWLLSSLCLL---LPDE 120
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      235 KVKAFLDQKCPFKAEPRFGQPAGEAEFLSSIR-----AYLMNRQAVLDETHLPDI 285
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY      121 DALPFLTLASAPSDGKTEAPRGAW 145
      ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      286 DALVELAASGDPTLPDPSLENPHAAW 310
      ||| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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Search completed: February 8, 2005, 13:42:10
Job time : 24.5458 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:32:20 ; Search time 66.4599 Seconds
(without alignment)
975.246 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDSYG.....WAHLGVQVWRACPCQVFKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/prodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
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19: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/prodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1059	99.8	199	10	US-09-816-653A-2
2	1048	98.8	487	16	US-10-362-240-2
3	1048	98.8	667	9	US-09-759-056-2
4	1048	98.8	667	9	US-09-901-812-2
5	1048	98.8	667	10	US-09-863-776-67
6	1048	98.8	667	14	US-10-227-884-80
7	1048	98.8	667	14	US-10-230-163-80
8	1048	98.8	667	14	US-10-230-338-80
9	1048	98.8	667	14	US-10-218-631-80
10	1048	98.8	667	14	US-10-230-414-80
11	1048	98.8	667	14	US-10-232-224-80
12	1048	98.8	667	14	US-10-216-159A-80
13	1048	98.8	667	14	US-10-218-849-80

14	1048	98.8	667	14	US-10-227-873-80	Sequence 80, Appl
15	1048	98.8	667	14	US-10-227-883-80	Sequence 80, Appl
16	1048	98.8	667	14	US-10-219-076-80	Sequence 80, Appl
17	1048	98.8	667	14	US-10-230-434-80	Sequence 80, Appl
18	1048	98.8	667	14	US-10-219-003-80	Sequence 80, Appl
19	1048	98.8	667	14	US-10-219-075-80	Sequence 80, Appl
20	1048	98.8	667	14	US-10-219-464-80	Sequence 80, Appl
21	1048	98.8	667	14	US-10-219-466-80	Sequence 80, Appl
22	1048	98.8	667	14	US-10-219-479-80	Sequence 80, Appl
23	1048	98.8	667	14	US-10-219-481-80	Sequence 80, Appl
24	1048	98.8	667	14	US-10-230-260-80	Sequence 80, Appl
25	1048	98.8	667	14	US-10-232-231-80	Sequence 80, Appl
26	1048	98.8	667	14	US-10-232-233-80	Sequence 80, Appl
27	1048	98.8	667	14	US-10-216-165-80	Sequence 80, Appl
28	1048	98.8	667	14	US-10-218-956-80	Sequence 80, Appl
29	1048	98.8	667	14	US-10-219-468-80	Sequence 80, Appl
30	1048	98.8	667	14	US-10-219-478-80	Sequence 80, Appl
31	1048	98.8	667	14	US-10-219-536-80	Sequence 80, Appl
32	1048	98.8	667	14	US-10-233-205-80	Sequence 80, Appl
33	1048	98.8	667	14	US-10-219-072-80	Sequence 80, Appl
34	1048	98.8	667	14	US-10-219-470-80	Sequence 80, Appl
35	1048	98.8	667	14	US-10-219-524-80	Sequence 80, Appl
36	1048	98.8	667	14	US-10-219-528-80	Sequence 80, Appl
37	1048	98.8	667	14	US-10-227-880-80	Sequence 80, Appl
39	1048	98.8	667	14	US-10-227-881-80	Sequence 80, Appl
40	1048	98.8	667	14	US-10-227-882-80	Sequence 80, Appl
41	1048	98.8	667	14	US-10-230-436-80	Sequence 80, Appl
42	1048	98.8	667	14	US-10-232-223-80	Sequence 80, Appl
43	1048	98.8	667	14	US-10-232-225-80	Sequence 80, Appl
44	1048	98.8	667	14	US-10-232-227-80	Sequence 80, Appl
45	1048	98.8	667	14	US-10-232-229-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-816-653A-2
; Sequence 2, Application US/09816653A
; Publication No. US20030021788A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Pennica, Diane
; TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE SA.
; FILE REFERENCE: 10716/57
; CURRENT APPLICATION NUMBER: US/09/816,653A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,532
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens hSTRA6 amino terminal polypeptide fragment
; FEATURES:
; NAME/KEY: MISC FEATURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: Xaa is any amino acid
US-09-816-653A-2

Query Match	99.8%	Score 1059;	DB 10;	Length 199;
Best Local Similarity	100.0%	Pred. No. 1.4e-96;		
Matches 199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSQPAGNQTSPGATEDSYG	SWIDBPQGXELQPEGEVPSCHTSIPPGYHACLASLSI	60
Db	1	MSQPAGNQTSPGATEDSYG	SWIDBPQGXELQPEGEVPSCHTSIPPGYHACLASLSI	60
Qy	61	LVLLLLAMLVRRQLWPDVCRGRLPSVDVDFLAGDPRAVPAVFWLLSSLCLLLPDE	120	
Db	61	LVLLLLAMLVRRQLWPDVCRGRLPSVDVDFLAGDPRAVPAVFWLLSSLCLLLPDE	120	

QY 121 DALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 180
Db 121 DALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 180
QY 181 AHLGVQVWORAECPQVPKI 199
Db 181 AHLGVQVWORAECPQVPKI 199

RESULT 2

US-10-362-240-2
; Sequence 2, Application US/10362240
; Publication No. US20040185442A1
; GENERAL INFORMATION:
; APPLICANT: MAO, Yumin
; APPLICANT: XIE, Yi
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE - HUMAN RETINOIC ACID-RESPONSIVE PROTEIN 53.5
; FILE REFERENCE: 011241.52054US
; CURRENT APPLICATION NUMBER: US/10/362,240
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/CN01/01252
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 00119715.0
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-240-2

Query Match 98.8%; Score 1048; DB 16; Length 487;
Best Local Similarity 99.0%; Pred. No. 5e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
Db 63 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 181
Db 123 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 182
QY 182 HLGQVQVWORAECPQVPKI 199
Db 183 HLGQVQVWORAECPQVPKI 200

RESULT 3

US-09-759-056-2
; Sequence 2, Application US/09759056
; Patent No. US20020156252A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. US20020156252A1el STRA6 Polypeptides
; FILE REFERENCE: GENENT.2827A2
; CURRENT APPLICATION NUMBER: US/09/759,056
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/197089
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/175849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/228914
; PRIOR FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-759-056-2

Query Match 98.8%; Score 1048; DB 9; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
Db 63 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 181
Db 123 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 182
QY 182 HLGQVQVWORAECPQVPKI 199
Db 183 HLGQVQVWORAECPQVPKI 200

RESULT 4

US-09-901-812-2
; Sequence 2, Application US/09901812
; Patent No. US20020173461A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Polakis, Paul
; APPLICANT: Szeto, Wayne
; TITLE OF INVENTION: UPREGULATION OF TUMOR ANTIGENS TO
; FILE REFERENCE: GENENT.083A
; CURRENT APPLICATION NUMBER: US/09/901,812
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/228,914
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/759,056
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/175,849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/197,089
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-812-2

Query Match 98.8%; Score 1048; DB 9; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYGSWVIDEPQGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
Db 63 VLLLLAMLVRRRLQWPCDVRGPGPLSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 181
Db 123 ALPFLTLASAPSDGKTEAPRGAMKILGLFHYAALYPLAACATAGHTAAHLGSLTSLW 182

QY 182 HLGQVQWQRAECQVPVKI 199
Db 183 HLGQVQWQRAECQVPVKI 200

RESULT 5
US-09-863-776-67
; Sequence 67, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Mishra, Vishnu
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Li, Li
; APPLICANT: Taupier, Raymond J
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: No. US20030198953A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-020
; CURRENT APPLICATION NUMBER: US/09/863,776
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/206,679
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,688
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,829
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/207,748
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/207,798
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/208,263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/208,831
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/209,451
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/210,060
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/219,507
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/221,337
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/221,927
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/263,135
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,688
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,694
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-863-776-67

Query Match 98.8%; Score 1048; DB 10; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQPAGNQTSGATEDYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASISIL 61
Db 3 SQPAGNQTSGATEDYSGWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACIASISIL 62

QY 62 VLLLLAMLVRRRQLWPCVRCRPGLPSPVDFLAGDRPRRAVPAAVFMVLLSSICLLLPDSD 121
Db 63 VLLLLAMLVRRRQLWPCVRCRPGLPSPVDFLAGDRPRRAVPAAVFMVLLSSICLLLPDSD 122

QY 122 ALPFLTLASAPSDQKTEAPRGANKILGLFHYAALYYPFLAACATAGHTAAHLLGSLTSLWA 181
Db 123 ALPFLTLASAPSDQKTEAPRGANKILGLFHYAALYYPFLAACATAGHTAAHLLGSLTSLWA 182

QY 182 HLGQVQWQRAECQVPVKI 199
Db 183 HLGQVQWQRAECQVPVKI 200

RESULT 6
US-10-227-884-80
; Sequence 80, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17

; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-08-04
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; PRIOR FILING DATE: 1998-08-17
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; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/108787
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108801

; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113296
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115565
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
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; PRIOR FILING DATE: 1999-03-23
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; PRIOR FILING DATE: 1999-03-29
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; PRIOR FILING DATE: 1999-04-05
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; PRIOR FILING DATE: 1999-04-21
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; PRIOR FILING DATE: 1999-04-26
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; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. NO. 7.3e-95;

Db 3 SOPAGNOTSPGATEDSYGSWIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 121
Db 63 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLLGSLTSLWA 181
Db 123 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLLGSLTSLWA 182
QY 182 HLGQVQWQRAECPOVPKI 199
Db 183 HLGQVQWQRAECPOVPKI 200

RESULT 11

US-10-232-224-80
; Sequence 80, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC11
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SOPAGNOTSPGATEDSYGSWIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYGSWIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 121

Db 63 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 122
QY 122 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLLGSLTSLWA 181
Db 123 ALPFLTLASAPSDGKTEAPRGAWKILGLFYHAALYYPLAACATAGHTAAHLLGSLTSLWA 182
QY 182 HLGQVQWQRAECPOVPKI 199
Db 183 HLGQVQWQRAECPOVPKI 200

RESULT 12

US-10-216-159A-80
; Sequence 80, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 SOPAGNOTSPGATEDSYGSWIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYGSWIDEPQGGEELOPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 121
Db 63 VLLLLAMLVRRRLQWPCVRCRPGLPSPVDFLAGDRPRAVPAAPVFWVLLSSICLLLPDED 122

; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 60/106464
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
; PRIOR FILING DATE: 1998-11-03
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; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 60/108849
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/112422
; PRIOR FILING DATE: 1998-12-15
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; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115558
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/115733
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/123618
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/125259
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 60/125775
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/126773
; PRIOR FILING DATE: 1999-03-29
; PRIOR APPLICATION NUMBER: 60/127887

; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131445
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/140650
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/140723
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SQPAGNQTSPGATEDSYGSHWYDEPOGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SQPAGNQTSPGATEDSYGSHWYDEPOGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLMLVRRRLQWPCVRCRGLPSVDFLAGDRPRAVPAAVFMVLLSLCLLLPDED 121
Db 63 VLLLLMLVRRRLQWPCVRCRGLPSVDFLAGDRPRAVPAAVFMVLLSLCLLLPDED 122
QY 122 ALPFLTLASAPSDQKTEAPRGAWKILGLFYAALYPLAACATAGHTAAHLGLSTLSWA 181
Db 123 ALPFLTLASAPSDQKTEAPRGAWKILGLFYAALYPLAACATAGHTAAHLGLSTLSWA 182
QY 182 HLGQVQWQRAECPOVPKI 199
Db 183 HLGQVQWQRAECPOVPKI 200

RESULT 15
US-10-227-883-80
; Sequence 80, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C78
CURRENT APPLICATION NUMBER: US/10/227,883
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/095302
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095318
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095916
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
PRIOR FILING DATE: 1998-08-11
PRIOR APPLICATION NUMBER: 60/096791
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/097986
PRIOR FILING DATE: 1998-08-26
PRIOR APPLICATION NUMBER: 60/098544
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/099596
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PRIOR APPLICATION NUMBER: 60/099803
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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100038
PRIOR FILING DATE: 1998-09-11
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100627
PRIOR FILING DATE: 1998-09-16
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PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/101477
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PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786
PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905
PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801
PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259
PRIOR FILING DATE: 1999-03-19

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 13:29:35 ; Search time 19.3683 Seconds
(without alignments)
988.580 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPNQTSFGATEDSYG.....WAHLGVQVWRAECQPVPKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: Pirl: *
2: Pirl2: *
3: Pirl3: *
4: Pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	86.5	8.2	757	2 F87304	beta-N-acetylhexos
2	85.5	8.1	380	2 S35785	glycoprotein I - b
3	84.5	8.0	335	2 T36304	probable anthranil
4	84	7.9	913	2 A48280	receptor tyrosine
5	83	7.8	1172	2 T36053	probable ABC-type
6	80.5	7.6	385	2 E83506	probable MFS trans
7	80	7.5	433	1 VHVUPH	nucleocapsid prote
8	80	7.5	876	2 A49508	protein-tyrosine k
9	80	7.5	921	2 G02326	transcription fact
10	79.5	7.5	249	1 S47153	type IV prepilin p
11	79.5	7.5	577	2 S77115	cytochrome c-type
12	79	7.4	463	2 C47301	virB6 homolog - Bo
13	79	7.4	910	2 A53137	tyrosine kinase re
14	78.5	7.4	477	2 H83588	probable MFS trans
15	78.5	7.4	532	2 JC5412	epidermal growth f
16	78.5	7.4	3519	2 S43048	polyketide synthas
17	78	7.4	419	2 JQ2254	farnesyl-diphospha
18	77.5	7.3	519	2 S35237	cytochrome c-type
19	77	7.3	521	2 AF3287	thiamine transport
20	76.5	7.2	221	2 B48266	protein-tyrosine k
21	76	7.2	394	2 A55045	probable 3-hydroxy
22	76	7.2	665	2 P83340	hypothetical prote
23	76	7.2	709	2 P75584	hypothetical prote
24	75.5	7.1	400	2 T35334	probable membrane
25	75.5	7.1	454	2 T10525	cyclin B1b-11 - ye
26	75.5	7.1	655	1 A42420	L-iduronidase (EC
27	75	7.1	211	2 T09498	cytochrome c bioge
28	75	7.1	230	2 S72714	Lepb1170 F2.64 pro
29	75	7.1	668	2 T01685	crpl protein - mai

30	74.5	7.0	425	2 C87619	hypothetical prote
31	74	7.0	320	2 A82449	conserved hypothet
32	73.5	6.9	233	2 T47136	hypothetical prote
33	73.5	6.9	300	2 D83487	hypothetical prote
34	73.5	6.9	636	2 JW0047	class I cyto kinase
35	73.5	6.9	1174	2 AH0663	probable pyruvate-
36	73.5	6.9	1201	2 A83007	hypothetical prote
37	73	6.9	411	2 D72588	hypothetical prote
38	73	6.9	473	2 T03611	cyclin, B-type - c
39	73	6.9	633	2 F84564	probable protein k
40	73	6.9	739	2 A83015	primosomal protein
41	73	6.9	786	2 F70735	hypothetical prote
42	72.5	6.8	176	2 B83199	hypothetical prote
43	72.5	6.8	258	2 S75950	hypothetical prote
44	72.5	6.8	529	2 C70545	hypothetical prote
45	72.5	6.8	636	1 VCVWFS	env polyprotein -

ALIGNMENTS

RESULT 1

F87304
beta-N-acetylhexosaminidase, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87304
R.Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo-
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87304
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-757 <STO>
A:Cross-references: UNIPROT:Q9AAZ5; GB:AE005673; NID:gl3421618; PIDN:AAK2434.1; GSPDB:
C:Genetics:
A:Gene: CC0447

Query Match		8.2%	Score 86.5;	DB 2;	Length 757;
Best Local Similarity		30.6%	Pred. No. 3.7;		
Matches		49;	Conservative	16;	Mismatches 60; Indels 35; Gaps 9;
QY	62	VLLLLAMLVRR	QLWPDCVGRGPGLPSPVDFLAGDRP	-----RAVPA	103
Db	65	VALQLADLIQSRGFRKVEGPPADAIV	--LTRGPGAEAYKLDINAKGATIAAKRA	122	
QY	104	AVFMVLLSSICLLLPDEDALPFLTLASAPSDQDKTEAPRAWKILGLFHYAALYY	-----P	159	
Db	123	GLFYGMSLWQLATPDEAKGFPVALLAASIE	----DAPRFAPWR	--GLMVDSARHYQSLDT	175
QY	160	LAACATAGHTAAHLLGSTLSWAHLGVQVWRAECQPVPKI	199		
Db	176	LKAVIDA--MAAHKL--NTFHHVLVDQGW--RLKIKYPKL	211		

RESULT 2

S35785
glycoprotein I - bovine herpesvirus 1
C:Species: bovine herpesvirus 1
C:Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S35785
R.Audonnet, J.
submitted to the EMBL Data Library, June 1993
A:Reference number: S35782
A:Accession: S35785
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <AUD>
A:Cross-references: UNIPROT:Q08102; EMBL:Z23068; NID:g312185; PIDN:CAA80605.1; PID:g312
C:Superfamily: pseudorabies virus glycoprotein gp63

C;Keywords: glycoprotein

Query Match 8.1%; Score 85.5; DB 2; Length 380;
Best Local Similarity 27.6%; Pred. No. 2.2;
Matches 37; Conservative 12; Mismatches 38; Indels 47; Gaps 6;
QY 4 PAGNOTSPGATEDSYSGWYIDEPQGXELQPEGVPSCHTIPGLYHACLAS----LS 59
DB 256 PAGPTASPNASPRFSA-----AAPAAAAQAGDTPA-----RFRQJASILVPLC 302
QY 60 ILVLLLLAM-----LVRRQL-----WPCVGRGRLGPSV 90
DB 303 VLVLLLLALCAVTNCALERRLLPCSRVYKPRTCACGSGTCAGRPCCRGAAAPSAPTV 362
QY 91 DFLAGDRPRAVPA 104
DB 363 VAL-GSRPKAPPLA 375

RESULT 3
T36304
probable anthranilate phosphoribotransferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36304
R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
A;Accession: T36304
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-335 <SAU>
A;Cross-references: UNIPROT:Q924W9; EMBL:AL035654; PIDN: CAB38583.1; GSPDB: GN00070; SCOEID
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: trpD2; SCOEID: SCEB.05c
C;Superfamily: anthranilate phosphoribosyltransferase; trpD homology

Query Match 8.0%; Score 84.5; DB 2; Length 335;
Best Local Similarity 30.8%; Pred. No. 2.4;
Matches 36; Conservative 10; Mismatches 42; Indels 29; Gaps 5;
QY 81 RGRPGSLPVPDLGRPRAVPAVFMVLLSLCLLPDDELALPFLTLASAPSDGKTEA 140
DB 247 RSRPG-----DLAGD--RANNAVLRRLVLAG-----GRGPARDVVLN 283
QY 141 PRGAWKILGFHYALYPLAACATAGHTAAHLGLSTLSWAHLGVQVMQRAECPOVP 197
DB 284 AAAALRVAGVAGTWSGDLRLAASAVDGGAAAGLLD---RWAHAS---WQADLVEVP 334

RESULT 4
A48280
receptor tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 31-May-1995 #sequence_revision 31-May-1995 #text_change 09-Jul-2004
C;Accession: A48280
R;Johnson, J.D.; Edman, J.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681, 1993
A;Title: A receptor tyrosine kinase found in breast carcinoma cells has an extracellular
A;Reference number: A48280; MUID: 93296201; PMID: 8390675
C;Accession: A48280
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-913 <RES>
A;Cross-references: UNIPROT:Q08345; GB: I11315; NID: G403386; PIDN: AAA02866.1; PID: G403387
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discooidin I amino-ter
C;Keywords: ATP
F:30-185/Domain: discooidin I amino-terminal homology <DN1>
F:608-912/Domain: protein kinase homology <KIN>
F:616-624/Region: protein kinase ATP-binding motif

Query Match 7.9%; Score 84; DB 2; Length 913;

Best Local Similarity 22.7%; Pred. No. 7.7;
Matches 39; Conservative 20; Mismatches 73; Indels 40; Gaps 7;
QY 7 NOTSPGATEDSYSGWYIDEPQ---GXELQPEGVPSCHT-SIPPLGYHACLASLSIL 61
DB 370 NNSSPALGGTFFPAPWPPGPPPTNFSSLELEPRQQPVAKAEGSPTAILIGCLVAIILL 429
QY 62 VILLLAMLV-----RRQLWPD-----CVRGRGLPSPVDLF--- 93
DB 430 LLLIALLMLRLHWRLLSKAERYLEBELTVHLSVPGDITLNNRPGRPPEPPYQERPP 489
QY 94 AGDRPRAVPAVFMVLLSLCLLPDDELALPFLTLASAPSDGKTEAPRGAW 145
DB 490 RGNPFHSPAC-----VPGSALLSNFAYRLLATYARPPRGFG---PTTPAW 534

RESULT 5
T36053
probable ABC-type transport protein cydCD - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36053
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21595
A;Accession: T36053
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1172 <SAU>
A;Cross-references: UNIPROT:Q9ZBY5; EMBL:AL034355; PIDN: CAA22219.1; GSPDB: GN00070; SCOEID
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: cydCD; SCOEID: SCD78.14
C;Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv0194; ATP-binding

Query Match 7.8%; Score 83; DB 2; Length 1172;
Best Local Similarity 31.5%; Pred. No. 12;
Matches 45; Conservative 12; Mismatches 68; Indels 18; Gaps 5;
QY 55 LASISILVLLMLVRRRQLWPCVGRGRLGPSVDFLAGDRPRAVPAVFMVLLSLC 114
DB 874 LAFAEVLGLAVQYQR-VRRSAERYVEYLDAPFVPEVPRQAPFPVVVEGLA 932
QY 115 LLLP--DEDALPFLTL-----ASAPSDGKTEAPRGAWKILGLFHYALYVPLA-- 161
DB 933 ARHFGQDRDALAGLDLTLEQGRVAVVGVSGSKTTL---AQVLLRFLDSAGSYTLGV 989
QY 162 -ACATAGHTAAHLGLSTLSWAHL 183
DB 990 DAYALAGDDVRLVGLCAQDAHL 1012

RESULT 6
E83506
probable MFS transporter PA1108 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83506
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID: 20437337; PMID: 10984043
A;Accession: E83506
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <STO>
A;Cross-references: UNIPROT:Q914M7; GB: AE004541; GB: AE0047024; PIDN: AAG0449
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1108

Query Match 7.6%; Score 80.5; DB 2; Length 385;
Best Local Similarity 29.0%; Pred. No. 6.6; Mismatches 14; Indels 57; Gaps 13;
Matches 54; Conservative 14; Mismatches 14; Indels 57; Gaps 13;
QY 27 POGXELQPEGEVPSCHTSIPPGLYHACLASISILVLLMLVRRRQLWPCVGRP-- 84
DB 148 PLGGQWLADLGGHP-----AVPATLAVLASLAALWV---PAWPEP--RPIL 189
QY 85 -GLSPVDF-----LAGDEP---RAVPAVFMVLLSSLC-----LLLPEDALPF---LT 127
DB 190 ACTPEPATLAIPIRRVLADRPLOTRALLVAVLVFVFAAGFVMVGDLPGLGFWIGLA 249
QY 128 LASAPSQDG--KTEAPRGAWKI-----LGLFHYAALYYPLAACATAGHTAAHLGST--- 177
DB 250 IAIASGLALNRLPR--TWSARRVRLGL-----ALAAAGATAQTLLAAGVYA 297
QY 178 --LSWA 181
DB 298 EGLYNA 303
RESULT 7
VHVUPH
nucleocapsid protein N - Prospect Hill virus (strain PHV-1)
N:Alternate names: nucleoprotein N
C:Species: Prospect Hill virus
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C:Accession: A34681
R:Parrington, M.A.; Kang, C.Y.
Virology 175, 167-175, 1990
A:Title: Nucleotide sequence analysis of the S genomic segment of Prospect Hill virus: C
A:Reference number: A34681; MUID:9017212; PMID:2309440
A:Accession: A34681
A:Molecule type: Genomic RNA
A:Residues: 1-433 <PAR>
A:Cross-references: UNIPROT:P22047
C:Genetics:
A:Gene: N
A:Map position: segment S
C:Superfamily: Hantaan virus nucleocapsid protein
C:Keywords: nucleocapsid; nucleoprotein
Query Match 7.5%; Score 80; DB 1; Length 433;
Best Local Similarity 24.1%; Pred. No. 8.4; Mismatches 21; Indels 55; Gaps 6;
Matches 35; Conservative 21; Mismatches 21; Indels 55; Gaps 6;
QY 23 YDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASISILVLL-----LAMLVRRQLWPD 78
DB 178 YVSMPTAQSTMKAEELTPGRFTIVCGLPFAQIMARNIISPVNMGVIGFAFFVKD---WAD 234
QY 79 CVRG-----RGLPS-PVDFLAGDRPRAVPAVFMVLLSSLCLL-----LPDE 120
DB 235 KVKAFLDQKCPFLKABRPQCPAGEAFLSSIR-----AYLMNQAVLDETHLPDI 285
QY 121 DALPFLTLASPSQDGKTEAPRGAW 145
DB 286 DALVELAASGDPTLPDSLENPHAAW 310
RESULT 8
A49508
protein-tyrosine kinase (EC 2.7.1.112) trke precursor - human
C:Species: Homo sapiens (man)
C>Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: A49508; I36358; S37402
R:Di Marco, E.; Cutuli, N.; Guerra, L.; Cancedda, R.; De Luca, M.
J. Biol. Chem. 268, 24290-24295, 1993
A:Title: Molecular cloning of trke, a novel trk-related putative tyrosine kinase recept
A:Reference number: A49508; MUID:94043265; PMID:8226977
A:Accession: A49508
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-876 <DIA>

A:Cross-references: UNIPROT:Q08345; EMBL:X74979; NID:9400462; PIDN:CAA52915.1; PID:94004
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; diacoidin I amino-ter
C:Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F:30-185/Domain: diacoidin I amino-terminal homology <DN1>
F:571-875/Domain: protein kinase homology <KIN>
F:579-587/Region: protein kinase ATP-binding motif
Query Match 7.5%; Score 80; DB 2; Length 876;
Best Local Similarity 20.6%; Pred. No. 17; Mismatches 26; Indels 62; Gaps 9;
Matches 42; Conservative 26; Mismatches 26; Indels 62; Gaps 9;
QY 7 NOTSGATEDSYSGWYIDEPQ-----GXELOPEGEVPSCHT-SIPPGLYHACLASLSIL 61
DB 370 NNSSPALGGTFPPAPWPPGPPPTNFSSLELEPRGQPPVAKAEGSPTAILIGCLVAIIL 429
QY 62 VLLLLAMLV-----RRRLWPD-----CVRGRPLPSVDFLAGDR 97
DB 430 LLLIILMLLWRLHWRRLLSKAERRVLEELTVHLSVPGDTILINRRPGPREPPY-QEPR 488
QY 98 PRAVPAVFMVLLSSLC-----LLPDEDALPFLTLASAPSQDGKTEAPRGAWKI 147
DB 489 PRGNPPH-----SAPCVNGSAYSODYMEPEKPGAPLL---PPPPQN----- 527
QY 148 LGLFHYAALYYPLAACATAGHTAA 171
DB 528 -SVPHVAEADIVTLQGVTTGNTYA 550
RESULT 9
G02326
transcription factor NFAT1 isoform B - human
C:Species: Homo sapiens (man)
C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02326
R:luo, C.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01056
A:Accession: G02326
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-921 <LUO>
A:Cross-references: UNIPROT:Q13469; EMBL:U43341; NID:gl353773; PIDN:AACS0886.1; PID:gl3
C:Genetics:
A:Gene: NFAT1
Query Match 7.5%; Score 80; DB 2; Length 921;
Best Local Similarity 23.5%; Pred. No. 18; Mismatches 30; Indels 80; Gaps 15;
Matches 57; Conservative 30; Mismatches 30; Indels 80; Gaps 15;
QY 3 QPAGNOTSPGATEDSYSGWYIDEPQGX-----ELOPEGEV-PSCHTSIPPGLYHAC 54
DB 240 RPASRSSSPGAKRRHSCAALVALPFGASPQRSRSPQPSHVAQDHGS-PAG--YPP 296
QY 55 LASLSILVLLLLAMLVRR-----RQLW-----PDCVGRGP---GLP-----SPVDFLA--- 94
DB 297 VAGSAVIMDALNSLATDSPGIPPKWKTSPPDSPVSAAPSAGLPRHIYPAVEFLGPCE 356
QY 95 -GDRPRAVPAVFMVLLSSLCLLLPEDALPFLTL---ASAP-----SODG----- 136
DB 357 QGERRNSAPESILLVPPTWPKPLVP---AIPICSIPTVATSLPPLPPLSQQSGSYELRIE 413
QY 137 -----KTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLGSTLSWAHLGV 185
DB 414 VQPKPHRAHYETEGSRGAVK-----APTGHPVVQLHG-YMENKPLGL 456
QY 186 QVW 188
DB 457 QIF 459
RESULT 10
S47153
type IV preplin peptidase (EC 3.4.99.-) Bfpp - Escherichia coli

N:Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
 C:Species: Escherichia coli
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S47153; S70974
 R:Zhang, H.; Lory, S.; Donnerberg, M.S.
 A:Description: A plasmid encoded prepilin peptidase from enteropathogenic Escherichia coli submitted to the EMBL Data Library, June 1994
 A:Reference number: S47153
 A:Accession: S47153
 A:Molecule type: DNA
 A:Residues: 1-249 <ZHA>
 A:CROSS-references: UNIPROT:Q57382; EMBL:Z34464; NID:G499386; PIDN:CAA84229.1; PID:G499386
 R:Stone, K.D.; Zhang, H.Z.; Carlson, L.K.; Donnerberg, M.S.
 Mol. Microbiol. 20: 325-337, 1996
 A:Title: A cluster of fourteen genes from enteropathogenic Escherichia coli is sufficient for virulence
 A:Reference number: S70966; MUID:96310370; PMID:8733231
 A:Accession: S70974
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-249 <STO>
 A:CROSS-references: EMBL:Z68186; NID:g1122399; PIDN:CAA92334.1; PID:g1122408
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
 C:Genetics:
 A:Gene: bfpP
 C:Superfamily: type IV prepilin peptidase
 C:Keywords: hydrolase; methyltransferase; S-adenosylmethionine

Query Match 7.5%; Score 79.5; DB 1; Length 249;
 Best Local Similarity 25.8%; Pred. No. 5.2;
 Matches 41; Conservative 11; Mismatches 62; Indels 45; Gaps 6;

QY 22 WIDPQGGXELQPEGEVPSCHTSIP-----PGLYHACLASLS 59
 DB 60 WYLLPVLGYFL-CRGEQCYCHAKVPVRYPLTEFTICGVCVIFVFLGDRLYDAVIVSLL 118

QY 60 ILVLLLLAMLVRRRLQWPCVRG-----RPGLPSPVDFLAGDRPRAVPAAPVFMVLLS 111
 DB 119 FLCLVFLALIDLRENWLPACTVYPLFWAGMITPGFASDDKIFG-----AFTGFLIMYISM 174

QY 112 SLCLLPDEDALPFTLTAAPSQDGKTEAPRGAWKILGL 150
 DB 175 KLVSALRKEDVPAGGDIALATA-----AGAW--LGI 203

RESULT 11
 S77715
 cytochrome c-type biogenesis protein homolog - evening primrose mitochondrion
 C:Species: mitochondrion Oenothera villaricae (evening primrose)
 C>Date: 06-Sep-1996 #sequence_revision 09-May-1997 #text_change 24-Sep-1999
 C:Accession: S77715; S35238; S77730
 R:Schuster, W.; Combettes, B.; Flieger, K.; Brennicke, A.
 Mol. Gen. Genet. 239, 49-57, 1993
 A:Title: A plant mitochondrial gene encodes a protein involved in cytochrome c biogenesis
 A:Reference number: S35237; MUID:93288005; PMID:8389979
 A:Accession: S77715
 A:Molecule type: mRNA
 A:Residues: 1-577 <SCH>
 A:CROSS-references: EMBL:X69555
 A:Note: the source is designated as Oenothera berteriana
 A:Note: 10-Ser, 13-Leu, 33-Leu, 46-Leu, 48-Cys, 51-Ser, 86-Trp, 88-Leu, 106-Leu, 112-Tyr, 113-Cys, 259-Leu, 263-Leu, 268-Leu, 306-Trp, 325-Phe, 368-Leu, 424-Trp, 433-Leu, 439-Tyr, 440-Cys, 441-Leu, 442-Leu, 443-Leu, 444-Leu, 445-Leu, 446-Leu, 447-Leu, 448-Leu, 449-Leu, 450-Leu, 451-Leu, 452-Leu, 453-Leu, 454-Leu, 455-Leu, 456-Leu, 457-Leu, 458-Leu, 459-Leu, 460-Leu, 461-Leu, 462-Leu, 463-Leu, 464-Leu, 465-Leu, 466-Leu, 467-Leu, 468-Leu, 469-Leu, 470-Leu, 471-Leu, 472-Leu, 473-Leu, 474-Leu, 475-Leu, 476-Leu, 477-Leu, 478-Leu, 479-Leu, 480-Leu, 481-Leu, 482-Leu, 483-Leu, 484-Leu, 485-Leu, 486-Leu, 487-Leu, 488-Leu, 489-Leu, 490-Leu, 491-Leu, 492-Leu, 493-Leu, 494-Leu, 495-Leu, 496-Leu, 497-Leu, 498-Leu, 499-Leu, 500-Leu, 501-Leu, 502-Leu, 503-Leu, 504-Leu, 505-Leu, 506-Leu, 507-Leu, 508-Leu, 509-Leu, 510-Leu, 511-Leu, 512-Leu, 513-Leu, 514-Leu, 515-Leu, 516-Leu, 517-Leu, 518-Leu, 519-Leu, 520-Leu, 521-Leu, 522-Leu, 523-Leu, 524-Leu, 525-Leu, 526-Leu, 527-Leu, 528-Leu, 529-Leu, 530-Leu, 531-Leu, 532-Leu, 533-Leu, 534-Leu, 535-Leu, 536-Leu, 537-Leu, 538-Leu, 539-Leu, 540-Leu, 541-Leu, 542-Leu, 543-Leu, 544-Leu, 545-Leu, 546-Leu, 547-Leu, 548-Leu, 549-Leu, 550-Leu, 551-Leu, 552-Leu, 553-Leu, 554-Leu, 555-Leu, 556-Leu, 557-Leu, 558-Leu, 559-Leu, 560-Leu, 561-Leu, 562-Leu, 563-Leu, 564-Leu, 565-Leu, 566-Leu, 567-Leu, 568-Leu, 569-Leu, 570-Leu, 571-Leu, 572-Leu, 573-Leu, 574-Leu, 575-Leu, 576-Leu, 577-Leu, 578-Leu, 579-Leu, 580-Leu, 581-Leu, 582-Leu, 583-Leu, 584-Leu, 585-Leu, 586-Leu, 587-Leu, 588-Leu, 589-Leu, 590-Leu, 591-Leu, 592-Leu, 593-Leu, 594-Leu, 595-Leu, 596-Leu, 597-Leu, 598-Leu, 599-Leu, 600-Leu, 601-Leu, 602-Leu, 603-Leu, 604-Leu, 605-Leu, 606-Leu, 607-Leu, 608-Leu, 609-Leu, 610-Leu, 611-Leu, 612-Leu, 613-Leu, 614-Leu, 615-Leu, 616-Leu, 617-Leu, 618-Leu, 619-Leu, 620-Leu, 621-Leu, 622-Leu, 623-Leu, 624-Leu, 625-Leu, 626-Leu, 627-Leu, 628-Leu, 629-Leu, 630-Leu, 631-Leu, 632-Leu, 633-Leu, 634-Leu, 635-Leu, 636-Leu, 637-Leu, 638-Leu, 639-Leu, 640-Leu, 641-Leu, 642-Leu, 643-Leu, 644-Leu, 645-Leu, 646-Leu, 647-Leu, 648-Leu, 649-Leu, 650-Leu, 651-Leu, 652-Leu, 653-Leu, 654-Leu, 655-Leu, 656-Leu, 657-Leu, 658-Leu, 659-Leu, 660-Leu, 661-Leu, 662-Leu, 663-Leu, 664-Leu, 665-Leu, 666-Leu, 667-Leu, 668-Leu, 669-Leu, 670-Leu, 671-Leu, 672-Leu, 673-Leu, 674-Leu, 675-Leu, 676-Leu, 677-Leu, 678-Leu, 679-Leu, 680-Leu, 681-Leu, 682-Leu, 683-Leu, 684-Leu, 685-Leu, 686-Leu, 687-Leu, 688-Leu, 689-Leu, 690-Leu, 691-Leu, 692-Leu, 693-Leu, 694-Leu, 695-Leu, 696-Leu, 697-Leu, 698-Leu, 699-Leu, 700-Leu, 701-Leu, 702-Leu, 703-Leu, 704-Leu, 705-Leu, 706-Leu, 707-Leu, 708-Leu, 709-Leu, 710-Leu, 711-Leu, 712-Leu, 713-Leu, 714-Leu, 715-Leu, 716-Leu, 717-Leu, 718-Leu, 719-Leu, 720-Leu, 721-Leu, 722-Leu, 723-Leu, 724-Leu, 725-Leu, 726-Leu, 727-Leu, 728-Leu, 729-Leu, 730-Leu, 731-Leu, 732-Leu, 733-Leu, 734-Leu, 735-Leu, 736-Leu, 737-Leu, 738-Leu, 739-Leu, 740-Leu, 741-Leu, 742-Leu, 743-Leu, 744-Leu, 745-Leu, 746-Leu, 747-Leu, 748-Leu, 749-Leu, 750-Leu, 751-Leu, 752-Leu, 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A:Molecule type: DNA
A:Residues: 1-910 <RES>
A:Cross-references: UNIPROT:Q63474; GB:I26525; NID:Q432480; PIDN:AAA21089.1; PID:Q432481
C:Genetics:
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C:Keywords: ATP
F:31-186/Domain: discoidin I amino-terminal homology <DNI>
F:605-909/Domain: protein kinase homology <KIN>
F:613-621/Region: protein kinase ATP-binding motif

Query Match 7.4%; Score 79; DB 2; Length 910;
Best Local Similarity 22.1%; Pred. No. 22;
Matches 36; Conservative 23; Mismatches 70; Indels 34; Gaps 7;

QY 13 ATEDYSYGSWYDEPO-----GGXELQPEGEVPSCHT-STPPGLYHACLASLSILVLLLLA 67
DB 373 SSDTTPAPWPPGPPPTNFSSLEPRGQQPVAKAEGSPTAILIGCLVAIILLLLIIIA 432
QY 68 MLV-----RRRLMPD-----CVRGRPGLPSPVDFLAGDRPRAVPA 103
DB 433 LMLRLHWRLLSKAERRVLEBELTVHLSVPGDTILNNRPGPREPPY-QEPRRGTTT 491
QY 104 AVFWLLSSLLCLLPED-ALPPLTLASAPSDGKTEAPRGAW 145
DB 492 HSAPCVPGNSALLSNPAYELLATYAPRPGG---PPTPAW 531

RESULT 14
H83588
Probable MFS transporter PA0458 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: H83588
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337; PMID:10984043
A:Accession: H83588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-477 <STO>
A:Cross-references: UNIPROT:Q9I660; GB:AE004483; GB:AE004091; NID:G9946313; PIDN:ARG0384
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0458
C:Superfamily: multidrug-efflux transporter

Query Match 7.4%; Score 78.5; DB 2; Length 477;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 54; Conservative 16; Mismatches 63; Indels 71; Gaps 11;

QY 19 YGSWY---IDEPG-----GXELOPE--GEVPSCHTSIPPGLYHACLASLSI----- 60
DB 164 YASWHWIFLNLPGVLGCLVAKMLPDLRSVPSPRDSIGFLLFGSMVLISIALEGLG 223
QY 61 -----LVLLIAMLVRRRLQMPDCVR-GRFGLSPVDFLAGDRPRAVPAVFWY-LL 110
DB 224 ELHLSHLRVLLIGLVLLTAYWLRALRIDKPLFP-----PSLFKARTFAVGIL 273
QY 111 SSLCLLLPDDALPFLT-----LASAPSDGKTEAPRG-----AWKILGLPHYA 154
DB 274 GNLFARL-GSGALPFLTPLLQVGLGYPPSTAGTMTIFLALFAMVAKPMAPKLLIDFFGYR 332
QY 155 ALYYPLAACATAGTAAHLLGSTL 178
DB 333 KL-----LVGNLTL 340

RESULT 15
JC5412

epidermal growth factor receptor-binding protein GRB-7 - human
C:Species: Homo sapiens (man)
C:Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5412
R:Kishni, T.; Sasaki, H.; Akiyama, N.; Ishizuka, T.; Sakamoto, H.; Aizawa, S.; Sugimura,
Biochem. Biophys. Res. Commun. 232, 5-9, 1997
A:Title: Molecular cloning of human GRB-7 co-amplified with CABL and c-ERBB-2 in primary
A:Reference number: JC5412; MUID:97236270; PMID:9125150
A:Accession: JC5412
A:Molecule type: mRNA
A:Residues: 1-532 <KIS>
A:Cross-references: UNIPROT:Q14451; DBJ:D43772; NID:G601890; PIDN:BA07827.1; PID:G601
C:Comment: This protein contains a pleckstrin domain which mediates protein-protein int
C:Genetics:
A:Gene: GDB:GRB7
A:Cross-references: GDB:1297554; OMIM:601522
F:231-336/Domain: pleckstrin #status predicted <PLE>
F:432-532/Domain: SH2 #status predicted <SH2>

Query Match 7.4%; Score 78.5; DB 2; Length 532;
Best Local Similarity 28.3%; Pred. No. 14;
Matches 39; Conservative 12; Mismatches 62; Indels 25; Gaps 7;

QY 75 LMPDCVGRGRPGLPSPVDF-LAGDRPRAVPAVFWVLLSSLLCLLPDEDAL-----P 124
DB 17 LWP-APGTPPGTTPRPPDTPLPEEVKRSQ-----LLIPTTGKRLREERERRATSLPSIPNP 70
QY 125 FLTLASAPSDCKTEAPRGAWKIL---GLFHYAALYPLAAC---ATAGHTAAHLGGS 176
DB 71 FPELCSPSPSQSPILGGPSSARGLLPRDASRPHVKYSEDGACRSVEVAAGATARHVCEM 130
QY 177 TLSWAH-LGVQVWQRAEC 193
DB 131 LVQRAHALSDETWGLVEC 148

Search completed: February 8, 2005, 13:41:04
Job time : 21.8683 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:21:20 ; Search time 87.3473 Seconds
(without alignments)
1166.650 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPNQTSFGATEDSYSGV.....WAHLGVQVQWQRAECQVQPKI 199

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1048	98.8	667	Q8TB21	Q8tb21 homo sapien
2	1048	98.8	667	Q9BX79	Q9bx79 homo sapien
3	1048	98.8	708	Q7Z3U9	Q7z3u9 homo sapien
4	986.5	93.0	658	Q9BX78	Q9bx78 homo sapien
5	745	70.2	159	Q6PJF8	Q6pjf8 mus musculus
6	697	65.7	670	Q70491	Q70491 mus musculus
7	697	65.7	670	Q6DIA8	Q6dia8 mus musculus
8	488	46.0	560	Q7L9G1	Q7l9g1 mus musculus
9	427	40.2	137	Q8C442	Q8c442 mus musculus
10	337	31.8	238	Q6DG26	Q6dg26 brachydanio
11	99.5	9.4	293	Q7WE26	Q7we26 bordetella
12	96.5	9.1	293	Q7W325	Q7w325 bordetella
13	96.5	9.1	441	Q6ZNR9	Q6zn9 mus musculus
14	90.5	8.5	840	Q7N1K1	Q7n1k1 gloebacter
15	90.5	8.5	2527	Q7W6G2	Q7w6g2 bordetella
16	90	8.5	263	Y8K6	Q8su0 encephalito
17	89.5	8.4	750	Q9YQ39	Q9yq39 suid herpes
18	88.5	8.3	435	Q854B3	Q854b3 mycobacteri
19	87.5	8.2	318	Q7NTK1	Q7ntk1 chromobacte
20	87.5	8.2	336	Q94LD3	Q94ld3 oryza sativ
21	87.5	8.2	413	Q8XRV5	Q8xrv5 ralstonia s
22	87	8.2	848	Q84SK5	Q84sk5 oryza sativ
23	86.5	8.2	757	Q9AAZ5	Q9aaz5 caulobacter
24	85.5	8.1	380	VGL1_BHVIS	Q8l02 bovine herp
25	85.5	8.1	569	Q8V1X8	Q8v1x8 ralstonia s
26	85	8.0	398	Q73UR0	Q73ur0 mycobacteri
27	84.5	8.0	335	TRD2_STRCO	Q8z4w9 streptomyc
28	84.5	8.0	382	Q39505	Q39505 bovine herp
29	84.5	8.0	382	Q76PFO	Q76pfo bovine herp
30	84.5	8.0	730	Q91QX7	Q91qx7 corynebacte
31	84.5	8.0	2527	Q7WID3	Q7wid3 bordetella

32 84 7.9 295 2 Q6ZJAB Q6zjab oryza sativ
33 84 7.9 909 1 DDRI_PANTR DDRI_PANTR
34 84 7.9 913 1 DDRI_HUMAN DDRI_HUMAN
35 84 7.9 917 2 Q67M4 Q67m4 sus scrofa
36 83.5 7.9 482 2 Q6Z576 Q6z576 oryza sativ
37 83 7.8 281 1 CBBE_RAT Cbbe_rat
38 83 7.8 344 2 Q7WMZ6 Q7wmz6 bordetella
39 83 7.8 496 2 Q72HN1 Q72hnl thermus the
40 83 7.8 1172 2 Q9ZBY5 Q9zby5 streptomyc
41 82 7.7 208 2 Q6Z437 Q6z437 laasea sp.
42 82 7.7 281 2 Q6PZD9 Q6pzd9 mus musculu
43 82 7.7 333 2 Q7WBH4 Q7wbh4 bordetella
44 82 7.7 2641 2 Q9BXD4 Q9bx4d homo sapien
45 81.5 7.7 521 2 Q7NT97 Q7nt97 chromobacte

ALIGNMENTS

RESULT 1

Q8TB21 PRELIMINARY; PRT; 667 AA.
AC Q8TB21;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stimulated by retinoic acid gene 6.
GN Name=FLJ12541;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025256; AAH25256.1; -;
SQ SEQUENCE 667 AA; 73532 MW; 120685F4635CB085 CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 667;

Best Local Similarity 99.0%; Pred. No. 6.9e-88;

Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SOPAGNQTSPGATEDSYSGSWYIDEPQGXELQEGEVPSCHTSIPFGLYHACIASLSIL 61

Db 3 SOPAGNQTSPGATEDSYSGSWYIDEPQGXELQEGEVPSCHTSIPFGLYHACIASLSIL 62

Qy 62 VLLLLAMLVRRRLQWLPCVGRGRLGSLFVDFLAGDRPRAVPAVFMVLLSSLCILLPDED 121

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Db 63 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 122
QY 122 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
Db 123 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 182
QY 182 HLGQVQWQRAECPOVPKI 199
Db 183 HLGQVQWQRAECPOVPKI 200

RESULT 2
Q9BX79 PRELIMINARY; PRT; 667 AA.
AC Q9BX79; Q9H9U8;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE STRA6 isoform 1
GN ORFNames=UNQ3126;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Marks M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF352728; RAK30289.1; -.
DR EMBL; AY359089; AAK9447.1; -.
SQ SEQUENCE 667 AA; 73502 MW; D20840A46998BA2E CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 667;
Best Local Similarity 99.0%; Pred. No. 6.9e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 3 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 62
QY 62 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 121
Db 63 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 122
QY 122 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
Db 123 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 182
QY 182 HLGQVQWQRAECPOVPKI 199
Db 183 HLGQVQWQRAECPOVPKI 199

RESULT 3
Q9BX79 PRELIMINARY; PRT; 708 AA.
AC Q9BX79;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Hypothetical protein DKFZp686P1959 (Fragment).
GN Name=DKFZp686P1959;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537413; CAD37655.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 708 AA; 77825 MW; DB88B84AEAD286ED CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 708;
Best Local Similarity 99.0%; Pred. NO. 7.3e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 44 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 103
QY 62 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 121
Db 104 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 163
QY 122 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
Db 164 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 223
QY 182 HLGQVQWQRAECPOVPKI 199
Db 224 HLGQVQWQRAECPOVPKI 241

RESULT 4
Q9BX79 PRELIMINARY; PRT; 658 AA.
AC Q9BX79;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE STRA6 isoform 2.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
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Db 183 HLGQVQWQRAECPOVPKI 200

RESULT 3
Q9BX79 PRELIMINARY; PRT; 708 AA.
AC Q9BX79;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Hypothetical protein DKFZp686P1959 (Fragment).
GN Name=DKFZp686P1959;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537413; CAD37655.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 708 AA; 77825 MW; DB88B84AEAD286ED CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 708;
Best Local Similarity 99.0%; Pred. NO. 7.3e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
Db 44 SOPAGNOTSPGATEDSYSGSWVIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 103
QY 62 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 121
Db 104 VLLLLAMLVRRQLPDCVGRGPGSPVDFLAGDRPRAVPAVFWLLSSLCILLPDED 163
QY 122 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 181
Db 164 ALPFLTASAPSDQKTEAPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWA 223
QY 182 HLGQVQWQRAECPOVPKI 199
Db 224 HLGQVQWQRAECPOVPKI 241

RESULT 4
Q9BX79 PRELIMINARY; PRT; 658 AA.
AC Q9BX79;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE STRA6 isoform 2.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
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RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA	Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.
RA	Lewis L., Liao D., Mark M.K., Robble E., Sanchez C., Schoenfeld J.,
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA	Vandlen R., Watanabe C., Wilead D., Woods K., Xie M.H., Yansura D.,
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA	Godowski P.;
RT	"the secreted protein discovery initiative (SPDI), a large-scale
RT	effort to identify novel human secreted and transmembrane proteins: a
RT	bioinformatics assessment."
RL	Genome Ref. 13:2265-2270(2003).
DR	EMBL; AF352729; AAK30290.1; -
DR	EMBL; AY358748; AAQ89108.1; -
SQ	SEQUENCE 658 AA, 72582 NW; 5405281727F647DD CRC64;
	Query Match 93.0%; Score 986.5; DB 2; Length 658;
	Best Local Similarity 94.4%; Pred. No. 3.le-82;
	Matches 187; Conservative 1; Mismatches 1; Indels 9; Gaps 1
QY	2 SOPAGNQTSPGATEDSYGSWVIDEPQGXELOPEGEVPSCHTNSIPGLHYACIASLSIL 61
DB	3 SOPAGNQTSPGATEDSYGSWVIDEPQGEELOPEGEVPSCHTNSIPGLHYACIASLSIL 62
QY	62 VLLLLAMLVRRRLQPLPDCVRGRGPLSPVDFLAGDRPRAPVAAFVMVLSSLCLLLPDED 121
DB	63 VLLLLAMLVRRRLQPLPDCVRGRGPLP-----RPRNPAAVFMLSSLCLLLPDED 113
QY	122 ALPFLTASAPSODGKTEAPRGAWKILGLFYAALTYPLAACATAGHTAAHLIGSTLSWA 181
DB	114 ALPFLTASAPSODGKTEAPRGAWKILGLFYAALTYPLAACATAGHTAAHLIGSTLSWA 173
QY	182 HLGVQVQWRAECPQVPKI 199
DB	174 HLGVQVQWRAECPQVPKI 191
RESULT 5	
ID	Q6PJF8 PRELIMINARY; PRT; 159 AA.
AC	Q6PJF8;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	FJL12541 protein.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Muscle;
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426030999;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Jordan H., Moore T., Wang J.J., Haieh F.,
RA	Hopkins R.F., Zedan B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Vallalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RT	"Generation and initial analysis of more than 15,000 full-length human

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66 LAMLVRRQLWPCVGRGPGVPSVDFLAGDRPRAPVPAVFWLSSCLLLPDEDALPF 125
67 LALLVRRRLWPCVGRGPGVPSVDFLAGDLSWTVPAAVFWLFSNCLLLPDPENPLPF 126
126 LTLASAPSDGKTEPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWAHLGV 185
127 LNLTAASSPDGEMETSRGPKLALLYYPALYYPPLAACASAGHQAFLGLTSLWAHLGV 186
186 QVWQRAECPQVPKI 199
187 QVWQRAECPQDPKI 200

RESULT 7
Q6DIA8 PRELIMINARY; PRT; 670 AA.
AC Q6DIA8, 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE StrA6 protein.
GN Mus musculus (Mouse)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek A., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073657; AAH73657.1; -
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 670 AA; 73715 MW; 96F963788EF91249 CRC64;

Query Match 65.7%; Score 697; DB 2; Length 670;
Best Local Similarity 68.6%; Pred. No. 1.4e-55;
Matches 133; Conservative 18; Mismatches 41; Indels 2; Gaps 1;

QY 6 GNQTSFGATEDSYSGWYIDEPGGXELQPEGEVPSCHTSIPPLVHACLASLILVLL 65
DB 9 GSQTSFGVDDYS-SWYIEPLGAEVQPEGVPLCQLTAPPALLHACLASLILVLL 66
66 LAMLVRRQLWPCVGRGPGVPSVDFLAGDRPRAPVPAVFWLSSCLLLPDEDALPF 125
67 LALLVRRRLWPCVGRGPGVPSVDFLAGDLSWTVPAAVFWLFSNCLLLPDPENPLPF 126
126 LTLASAPSDGKTEPRGAWKILGLFHYAALYYPPLAACATAGHTAAHLGSLTSLWAHLGV 185
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127 LNLTAASSPDGEMETSRGPKLALLYYPALYYPPLAACASAGHQAFLGLTSLWAHLGV 186
186 QVWQRAECPQVPKI 199
187 QVWQRAECPQDPKI 200

RESULT 8
Q7L9G1 PRELIMINARY; PRT; 560 AA.
AC Q7L9G1, 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ12541.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Sato K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosiiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura M., Takigami A.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujii Y.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RL cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK022603; BAB14122.1; -
SQ SEQUENCE 560 AA; 61987 MW; DF0FED7687AED74 CRC64;

Query Match 46.0%; Score 488; DB 2; Length 560;
Best Local Similarity 98.9%; Pred. No. 2e-36;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 107 MVLLSSCLLLPDEDALPFLTLASAPSDGKTEPRGAWKILGLFHYAALYYPPLAACATA 166
DB 1 MVLLSSCLLLPDEDALPFLTLASAPSDGKTEPRGAWKILGLFHYAALYYPPLAACATA 60
167 GHTAAHLGSLTSLWAHLGVQVWQRAECPQVPKI 199
DB 61 GHTAAHLGSLTSLWAHLGVQVWQRAECPQVPKI 93

RESULT 9
Q8C442 PRELIMINARY; PRT; 137 AA.
ID Q8C442
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Db 2 SAETVNNYSDWY---ENRAPTKAPVEVIPPCTDEGLFHICIAAISLVWMLVAIL 58
QY 70 VRRQLWPCVGRGFLSPVDLAGDRPRAPVAAVFMVLLSSCLLPDEALPFTLTA 129
Db 59 ARQKL-SDNQRLGLTLLSPVNFLDHTQKGLAVAVGVLFCKLVGMVLSHHPLPFT--- 114
QY 130 SAPSDGKTEAPRGAWKILGLFHYAALYYPLAACATAGTAAHLLGSLTSHAHLGVQVWQ 189
Db 115 -----KEVANKEFMILALLYPALYYPLIACGTLHNKVGYYLVGSLSTWTFHGLVWQ 167
QY 190 RAECQVVKI 199
Db 168 KVDCPKTQOI 177

RESULT 11
Q7WE26 PRELIMINARY; PRT; 293 AA.
AC Q7WE26;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames-BB4812;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640451; CAE35175.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6; 1.
KW Complete proteome.
SQ SEQUENCE 293 AA; 29783 MW; E66BA78D5E88CA0C CRC64;

Query Match 9.4%; Score 99.5; DB 2; Length 293;
Best Local Similarity 27.3%; Pred. No. 0.58;
Matches 50; Conservative 17; Mismatches 53; Indels 63; Gaps 9;
QY 43 HTSIPGLY---HACLAS--LSILVLLLLAMLVRRRLWPCVGRGFLSPVDLAGDR 97
Db 2 HVSAALPQAPARHAANGAVAAIILLWASLALMTATAQ-----GLP----- 41
QY 98 PRAPVAAVFMVLLSSCLLPDEALPFTLTAAPSQDGKTEAPRGAWKIL--GLPHYAA 155
Db 42 PFQLLAASFGVAFALSAVLL-----TARRAWGRRLRAPAGAWLLAVGGIFGYHA 89
QY 156 LYY-----PLAAC-----ATAGHTAAH-----LLGSTLSWAHLGVQVWQRA 191
Db 90 LYFVALGNAPVAEASLIAYLWPLLIIVLFALRGAGGARRWRALAGAALGFAGTALLVWQRA 149
QY 192 ECP 194
Db 150 GGP 152

RESULT 12
Q7W325 PRELIMINARY; PRT; 293 AA.
AC Q7W325;
DT 01-OCT-2003 (TremBLrel. 25, Created)
DT 01-OCT-2003 (TremBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE Putative membrane protein.
GN OrderedLocusNames-BPP4224;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrett B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640436; CAE39503.1; --
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR000620; DUF6.
DR Pfam; PF00892; DUF6; 1.
KW Complete proteome.
SQ SEQUENCE 293 AA; 29769 MW; 1C52078C7FF76A0E CRC64;

Query Match 9.1%; Score 96.5; DB 2; Length 293;
Best Local Similarity 26.8%; Pred. No. 1.1;
Matches 49; Conservative 17; Mismatches 54; Indels 63; Gaps 8;
QY 43 HTSIPGLYHACLAS-----LSILVLLLLAMLVRRRLWPCVGRGFLSPVDLAGDR 97
Db 2 HVSAALPQAPARHAANGAVAAIILLWASLALMTATAQ-----GLP----- 41
QY 98 PRAPVAAVFMVLLSSCLLPDEALPFTLTAAPSQDGKTEAPRGAWKIL--GLPHYAA 155
Db 42 PFQLLAASFGVAFALSAVLL-----TARRAWGRRLRAPAGAWLLAVGGIFGYHA 89
QY 156 LYY-----PLAAC-----ATAGHTAAH-----LLGSTLSWAHLGVQVWQRA 191
Db 90 LYFVALGNAPVAEASLIAYLWPLLIIVLFALRGAGGARRWRALAGAALGFAGTALLVWQRA 149
QY 192 ECP 194
Db 150 GGP 152

RESULT 13
Q6ZNR9 PRELIMINARY; PRT; 441 AA.
AC Q6ZNR9;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Hypothetical protein FLU27266.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Thymus;
RA Oshima A., Takahashi-Fujii A., Tanase T., Inose N., Takeuchi K.,
RA Arita M., Mushashino K., Yuuki H., Hara H., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130776; BAC85426.1; -.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Receptor.
SQ SEQUENCE 441 AA; 48434 MW; E43EDFC4753A0BB4 CRC64;

Query Match 9.1%; Score 96.5; DB 2; Length 441;
Best Local Similarity 24.1%; Pred. No. 1.7; 73; Indels 15; Gaps 5;
Matches 35; Conservative 22; Mismatches 22;

QY 7 NOTSPGATEDSYGWSVIDEPQ----GGXELQEGEVPSCHT-SIPPGLYHACLSLSIL 61
DB 101 NNSPALGCTFPAPWWPGPPPTNFSLEPRGQPVAKAGSGTALLIGCLVAIILL 160

QY 62 VLLLLAMLVNR----RLWPCVGRGCLSPVDFLAGDRPRAVPAVFWVLLSSCLLLP 118
DB 161 LLLIIALLMLRWLRLLSKVLESHPRTRSP--GLVGIRPTLPVSPFALRCCS-----P 213

QY 119 DEPALPFLTLASAPSDGKTEAPRG 143
DB 214 IQPTASFWPLTPVPLEARAPHPPG 238

RESULT 14
Q7NIKI Q7NIKI PRELIMINARY; PRT; 840 AA.
AC Q7NIKI;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G112182 protein.
GN OrderedLocustNames=g112182;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421;
RX MEDLINE=22977040; PubMed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yanada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; AP006575; BAC90123.1; -.
DR HSP; P50870; 1MR7.
DR GO; GO:0016747; F:transferase activity, transferring groups o...; IEA.
DR InterPro; IPR002656; Acyl_transf_3.
DR InterPro; IPR003018; GAP.
DR InterPro; IPR001451; Hexapep_transf.
DR InterPro; IPR011004; Trimer_lpXa_like.
DR Pfam; PF01757; Acyl_transf_3; 1.
DR Pfam; PF01590; GAP; 1.

DR Pfam; PF00132; Hexapep; 6.
DR PROSITE; PS00101; HEXAPEP_TRANSFERRASES; 1.
KW Complete proteome.
SQ SEQUENCE 840 AA; 90623 MW; 4C2A59EF60ABD838 CRC64;

Query Match 8.5%; Score 90.5; DB 2; Length 840;
Best Local Similarity 26.2%; Pred. No. 12;
Matches 53; Conservative 21; Mismatches 65; Indels 63; Gaps 13;

QY 26 EPQGXELQEGEVPSCHT-SIPPGLYHACLSLSILVLLAMLVRRRLQWPCVGRGPG 85
DB 14 EPRGDMTTEPKDPKPSLRHLVLDG-----LRGLTALYLFF-----HLWCD-LSFKPQ 60

QY 86 LPSPVDFLAGD-RPRAVPAA-----VFVLLSSCLLPLDEPDALPFLTLASAP 132
DB 61 LR-----LAGEPMPTWLQAAATAWAGYGLFSGVGFNV-LSGYCLMLP-----VV 102

QY 133 SQDGKTEA-----PRGAWKILGLFHYAALYYPPLAACATAGTAHLLG-----STLS 179
DB 103 RSDGRLRGVGTGKLRRAWRIILPPY-FAALGLSLVIALVAGAGSGQSLGYMWDKAMNGFT 161

QY 180 W-----AH-LGVQVWQRAECPQV 196
DB 162 WEGVLAHLLLVHNWSEQAQSTI 183

RESULT 15
Q7W6G2 Q7W6G2 PRELIMINARY; PRT; 2527 AA.
AC Q7W6G2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative type I polyketide synthase.
GN Name=wcBR; OrderedLocustNames=BFP2950;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Doggett J.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Davis K.,
RA Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
serine of the protein (by similarity).
CC -1- SIMILARITY: Contains 1 acyl carrier domain.
DR EMBL; BX640432; CAB38242.1; -.
DR HSP; P39435; 1KAS.
DR GO; GO:0000036; F:acyl carrier activity; IEA.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0004837; F:cofactor binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003231; Acyl_carrier.
DR InterPro; IPR001227; Ac_transferase.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000794; Ketoacyl_synth.

DR InterPro: IPR006163; Phosphateth_bind.
DR Pfam: PF00698; Acyl_transf_1; 1.
DR Pfam: PF00107; ADH_zinc_N; 1.
DR Pfam: PF00109; ketoacyl-synt; 1.
DR Pfam: PF02801; Ketoacyl-synt_C; 1.
DR Pfam: PF00550; PP-binding; 1.
DR ProDom: PD000887; Acyl_carrier; 1.
DR PROSITE; PS00075; ACP_DOMAIN; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Complete proteome; Phosphatetheine; Transferase.
SQ SEQUENCE 2527 AA; 269583 MW; 599CFAD9E3AE9985 CRC64;

Query Match 8.5%; Score 90.5; DB 2; Length 2527;
Best Local Similarity 29.0%; Pred. No. 36;
Matches 51; Conservative 16; Mismatches 66; Indels 43; Gaps 9;
QY 24 IDEPQGGXELQPEGEVPSC-HTSIPPG-----LYHA-----CLASLSI 60
DB 1423 IDEAEHLRRCFDLSVQAIDHTPEPAGRFDLAILHANWPTLDEARQALGHVHCLAPGGV 1482
QY 61 LVLLILLMLVRRQLWPDCVGRGRLPSVDFLAGD-RPRVPAAVFWVLLSSL-CL--- 115
DB 1483 LLL-----LANQPTAWLDFIFGARG-QWMSDSVAGDATPALQPAAFWRRELQALGCACEP 1536
QY 116 ---LLPDEDALPFL-----TLASAPSDQKTEAPRGAWKILGLFHYAALYYPLAA 162
DB 1537 AADFLPDTTRSGPYLLAATVATVADGSDGTVDAPPARRWLLLDADAADAAVARPLAA 1592

Search completed: February 8, 2005, 13:40:07
Job time : 90.3473 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 13:20:30 ; Search time 144.513 Seconds
(without alignments)
869.796 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYSALVLSCLTLFLVLMRS.....APPTWLWESQQGFWRKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	99.1	325	6 ABB99463	Abb99463 Amino aci
2	1134	66.9	660	5 AAU91277	Aau91277 Human NOV
3	1110.5	65.5	491	5 ABP68961	Abp68961 Human pol
4	1110.5	65.5	560	4 AAB94108	Aab94108 Human pro
5	1110.5	65.5	560	5 ABP69799	Abp69799 Human pol
6	1110.5	65.5	599	7 ADB64152	Adb64152 Human pro
7	1110.5	65.5	666	6 ABU82087	Abu82087 Novel hum
8	1110.5	65.5	667	4 AAU04557	Aau04557 Human Str
9	1110.5	65.5	667	4 AAU88572	Aau88572 Human hyd
10	1110.5	65.5	667	5 AAU83631	Aau83631 Human PRO
11	1110.5	65.5	667	5 AAU78575	Aau78575 Human Str
12	1110.5	65.5	667	5 ABB05048	Abb05048 Human NOV
13	1110.5	65.5	667	5 AAU019413	Aau019413 Human mol
14	1110.5	65.5	667	6 ABU80778	Abu80778 Human PRO
15	1110.5	65.5	667	6 ABO33744	Abo33744 Novel hum
16	1110.5	65.5	667	6 ABJ72267	Abj72267 Human PRO
17	1110.5	65.5	667	6 ABJ72395	Abj72395 Human PRO
18	1110.5	65.5	667	6 ABO34290	Abo34290 Human sec
19	1110.5	65.5	667	7 ABJ72097	Abj72097 Human mem
20	1110.5	65.5	667	7 ADB83570	Adb83570 Novel hum
21	1110.5	65.5	667	7 ADB80676	Adb80676 Novel hum
22	1110.5	65.5	667	7 ADB73217	Adb73217 Novel hum
23	1110.5	65.5	667	7 ADB78299	Adb78299 Novel hum
24	1110.5	65.5	667	7 ADB84947	Adb84947 Human PRO
25	1110.5	65.5	667	7 ADB78053	Adb78053 Novel hum

ALIGNMENTS

RESULT 1

ABB99463
ID ABB99463 standard; protein; 325 AA.

XX AC ABB99463;

XX DT 12-FEB-2003 (first entry)

XX DE Amino acid sequence of the carboxy-terminal of human STRA6.

XX KW Human; STRA6; retinoic acid; hSTRA6; Wnt-1; cellular transformation;

XX KM tumour; colon cancer; breast cancer; melanoma; gene therapy.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 146 /note= "unknown amino acid encoded by GNN"

FT Misc-difference 147 /note= "unknown amino acid encoded by NNN"

FT Misc-difference 148 /note= "unknown amino acid encoded by NCC"

FT Misc-difference 213 /note= "Gly encoded by GG"

FT Misc-difference 232 /note= "unknown amino acid encoded by ANG"

FT Misc-difference 290 /note= "unknown amino acid encoded by NGT"

FT Misc-difference 292 /note= "unknown amino acid encoded by TNG"

FT Misc-difference 302 /note= "unknown amino acid encoded by CAN"

FT Misc-difference 303 /note= "unknown amino acid encoded by GAN"

WO200277027-A1.

PD 03-OCT-2002.

XX 23-MAR-2001; 2001WO-US0009561.

XX 23-MAR-2000; 2000US-0191532P.

XX (CURA-) CURAGEN CORP.

XX (GETH) GENENTECH INC.

XX Rastelli LK, Pennica D;

DR WPI: 2003-059366/05.
 DR N-PSDB; ABV76853.
 XX
 PT New human STRA6 (stimulated by retinoic acid) proteins and nucleic acids
 PT encoding the proteins, useful for treating cancers (e.g. colon and breast
 PT cancer, or melanoma), or in gene therapy.
 XX
 PS Claim 4; Page 11-13; 11pp; English.
 XX
 CC The present sequence represents the carboxy-terminal portion of a human
 CC protein, designated STRA6 (stimulated by retinoic acid). hSTRA6 (human
 CC STRA6) is modulated by Wnt-1 and plays a role in cellular transformation.
 CC The hSTRA6 nucleic acids and proteins are useful for treating tumours
 CC (e.g. colon and breast cancer, or melanoma), in gene therapy, in
 CC diagnostic applications where the presence or amount of the nucleic acid
 CC or protein is to be assessed, and in the generation of antibodies that
 CC bind immunospecifically to these sequences for therapeutic and diagnostic
 CC applications. hSTRA6 nucleic acid fragments may be used as hybridization
 CC probes to identify hSTRA6-encoding nucleic acids, or as PCR primers for
 CC amplification and/or mutation of hSTRA6 molecules
 XX
 SQ Sequence 325 AA;
 Query Match 99.1%; Score 1679; DB 6; Length 325;
 Best Local Similarity 100.0%; Pred. No. 5,3e-166;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CYISALVLSCLTFLVLMRSVTHRLGGSGDGFNSVPLPLPPLAGLLVQIIF 60
 Db |||||
 QY 1 CYISALVLSCLTFLVLMRSVTHRLGGSGDGFNSVPLPLPPLAGLLVQIIF 60
 Db |||||
 QY 61 FLGTTALFLVLMPLVHGNLFFRSLESSWPFMTLALAVILQNNAAHWFLETHDGH 120
 Db |||||
 QY 61 FLGTTALFLVLMPLVHGNLFFRSLESSWPFMTLALAVILQNNAAHWFLETHDGH 120
 Db |||||
 QY 121 QLTNRRLVYAATFLFLPLNLVGMXXCSPSIAIRHPTGYYTYRNFLEKIEVSQHPAM 180
 Db |||||
 QY 121 QLTNRRLVYAATFLFLPLNLVGMXXCSPSIAIRHPTGYYTYRNFLEKIEVSQHPAM 180
 Db |||||
 QY 181 TAFCSLLQAOQLLPRTPMAOPDSLRPEDESGMQLLOKDSMAKARGPAGXRGARWGL 240
 Db |||||
 QY 181 TAFCSLLQAOQLLPRTPMAOPDSLRPEDESGMQLLOKDSMAKARGPAGXRGARWGL 240
 Db |||||
 QY 241 AYTLLHNPTLOVFRKLTALGANGAOPCSLPGSPSITPAMOPAGPDHGXGVEVLHWE 300
 Db |||||
 QY 241 AYTLLHNPTLOVFRKLTALGANGAOPCSLPGSPSITPAMOPAGPDHGXGVEVLHWE 300
 Db |||||
 QY 301 PXXGSAPPTWLWESQGGFWRKKLVG 325
 Db |||||
 QY 301 PXXGSAPPTWLWESQGGFWRKKLVG 325
 Db |||||
 RESULT 2
 AAU91277
 ID AAU91277 standard; protein; 660 AA.
 XX
 AC AAU91277;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human NOV2a protein.
 XX
 KW Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis; diabetes;
 KW cell signal processing; metabolic pathway modulation; inflammation;
 KW autoimmune disorder; scleroderma; transplantation; allergy;
 KW systemic lupus erythematosus; haemophilia; Alzheimer's disease;
 KW graft versus host disease; Lesch-Nyhan syndrome; periodontitis;
 KW pancreatitis; musculoskeletal disorder; Parkinson's disease;
 KW Huntington's disease; behavioural disorder; pain; obesity; wound healing;
 KW neurodegenerative disorder; neuropsychiatric disorder; hypertension;
 KW growth disorder; reproductive disorder; lung disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200216600-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 27-AUG-2001; 2001WO-US026518.
 XX
 PR 25-AUG-2000; 2000US-0227800P.
 PR 25-AUG-2000; 2000US-0228205P.
 PR 25-AUG-2000; 2000US-0228344P.
 PR 30-AUG-2000; 2000US-0228997P.
 PR 30-AUG-2000; 2000US-0229185P.
 PR 01-SEP-2000; 2000US-0229780P.
 PR 01-SEP-2000; 2000US-0229848P.
 PR 01-SEP-2000; 2000US-0229850P.
 PR 22-JAN-2001; 2001US-0263377P.
 PR 31-JAN-2001; 2001US-0265518P.
 PR 15-MAR-2001; 2001US-0276451P.
 PR 27-MAR-2001; 2001US-0279196P.
 PR 24-AUG-2001; 2001US-00939398.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 XX Gerlach V, Macdougall JR, Smithson G, Stone DJ, Ellerman K;
 PI Spytek KA, Zerhusen BD, Rastelli L, Verney CAM, Patturajan M;
 PI Tchernev VT, Padigar M, Taupier RJ;
 XX
 DR WPI; 2002-292064/33.
 DR N-PSDB; ABK55561.
 XX
 PT New isolated cytoplasmic, nuclear, membrane bound and secreted
 PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune
 PT disorders, hemophilia, Lesch-Nyhan syndrome, pancreatitis,
 PT musculoskeletal disorders.
 XX
 Claim 1; Page 18; 245pp; English.
 XX
 CC The invention relates to an isolated cytoplasmic, nuclear, membrane bound
 CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,
 CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a
 CC mature form, or a variant of the mature form of NOVX. Also included are a
 CC polynucleotide encoding NOVX (or its complement), a vector comprising the
 CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,
 CC determining the presence of NOVX in a sample using the antibody,
 CC determining the presence of NOVX polynucleotide in a sample using a probe
 CC which binds to NOVX polynucleotide, identifying an agent which binds to
 CC NOVX (including modulators of NOVX). NOVX, the polynucleotide and the
 CC antibody are useful for diagnosing, treating or preventing a NOVX-
 CC associated disorder selected from cardiomyopathy, atherosclerosis,
 CC diabetes, a disorder related to cell signal processing and metabolic
 CC pathway modulation, inflammation, autoimmune disorders, scleroderma,
 CC transplantation, allergies, systemic lupus erythematosus, haemophilia,
 CC graft versus host disease, Alzheimer's disease, stroke, Lesch-Nyhan
 CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders,
 CC Parkinson's disease, Huntington's disease, behavioural disorders, pain,
 CC neurodegenerative and neuropsychiatric disorders, hypertension, wound
 CC healing, obesity, growth and reproductive disorders, lung diseases and
 CC many other diseases and disorders listed in the specification. NOVX, the
 CC polynucleotide and the antibody are useful in screening assays, detection
 CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
 CC predictive medicine (e.g., diagnostic assays, prognostic assays,
 CC monitoring clinical trials and pharmacogenomic), and in methods of
 CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as
 CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to
 CC screen for potential agonist and antagonist compounds, and as bait
 CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is
 CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic
 CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is
 CC useful for producing non-human transgenic animals. The antibody is useful
 CC for isolating, and purifying NOVX and to monitor protein levels in tissue
 CC as part of a clinical testing procedure. The present sequence represents
 CC a NOVX protein
 XX

```
SQ      Sequence 660 AA;
Query Match      66.9%; Score 1134; DB 5; Length 660;
Best Local Similarity 76.9%; Pred. No. 8.4e-109;
Matches 237; Conservative 4; Mismatches 25; Indels 42; Gaps 5;

QY      1  CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB      353  CYISALVLSCLLTFLVLMRSLVTHRNLRALHARGAALDLSPLRSPHPSRQAIFCWMFS 412

QY      43  VLP-----LPPLAGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLT 97
DB      413  AYQTAFICLPLPLAGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLT 472

QY      98  ALAVILQNAHVVFLTHDGHQPOLNRRVLYAATFLFPLNVLVGAMVATRWVLLSALY 149
DB      473  ALAVILQNAHVVFLTHDGHQPOLNRRVLYAATFLFPLNVLVGAMVATRWVLLSALY 532

QY      150  -----SPSIATRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTM 198
DB      533  NAIHLGQMDLSLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTM 592

QY      199  AAPQSLRPGDEEGMQLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPVLQVFRKTAL 258
DB      593  AAPQSLRPGDEEGMQLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPVLQVFRKTAL 652

QY      259  LGANGAQP 266
DB      653  LGANGAQP 660

RESULT 3
ABP68961
ID      ABP68961 standard; protein; 491 AA.
AC
AC      ABP68961;
XX
XX
DT      20-JAN-2003 (first entry)
DE
DE      Human polypeptide SEQ ID NO 1008.
XX
XX      Human; genome mapping; gene therapy; food supplement; virus; fungus;
XX      cell-proliferative disorder; neurodegenerative disease; bacterial;
XX      Parkinson's disease; Alzheimer's disease; autoimmune disease;
XX      multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX      arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
XX      antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
XX      haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
XX      antiarthritic.
XX
XX      Homo sapiens.
XX
XX      WO200270539-A2.
XX
XX      12-SEP-2002.
XX
XX      05-MAR-2002; 2002WO-US005095.
XX
XX      05-MAR-2001; 2001US-00799451.
XX
XX      (HYSE-) HYSEQ INC.
XX
XX      Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
XX      Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
XX      Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX      WPI; 2002-759812/82.
XX
XX      N-PSDB; ABZ11178.
XX
XX      New polynucleotides comprising sequences assembled from expressed
XX      sequence tags (ESTs), useful for treating cell-proliferative,
XX      neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
XX      or coagulation disorders.
```

```
XX      Claim 9; SEQ ID NO 1008; 1012pp + Sequence Listing; English.
XX
XX      The invention relates to an isolated polynucleotide (I) comprising a
XX      nucleotide sequence selected from any of 948 sequences (ABZ11119-
XX      ABZ12066) or their mature protein coding portion, active domain coding
XX      protein or complementary sequences. The polynucleotides are useful for
XX      identifying expressed genes or for physical mapping of human genome. The
XX      encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
XX      markers, as a food supplement, for generating antibodies, in medical
XX      imaging, screening and diagnostic assays and for treating cell-
XX      proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
XX      or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
XX      diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
XX      platelet or coagulation disorders, wound, burns, incision, ulcers, liver
XX      or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
XX      arthritis, etc. Note: The sequence data for this patent did not form part
XX      of the printed specification, but was obtained in electronic format
XX      directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX      Sequence 491 AA;
Query Match      65.5%; Score 1110.5; DB 5; Length 491;
Best Local Similarity 76.6%; Pred. No. 1.6e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY      1  CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB      189  CYISALVLSCLLTFLVLMRSLVTHRNLRALHARGAALDLSPLRSPHPSRQAIFCWMFS 248

QY      43  VLPPLPPLAGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
DB      249  AYQTAFICLGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 308

QY      103  LQNAHVVFLTHDGHQPOLNRRVLYAATFLFPLNVLVGAMVATRWVLLSALYNAIHL 149
DB      309  LQNAHVVFLTHDGHQPOLNRRVLYAATFLFPLNVLVGAMVATRWVLLSALYNAIHL 368

QY      150  -SPSIATRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTM 203
DB      369  GQMDLSLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTM 428

QY      204  SLRPGDEEGMQLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPVLQVFRKTAL 263
DB      429  SLRPGDEEGMQLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPVLQVFRKTAL 488

QY      264  AQP 266
DB      489  AQP 491

RESULT 4
AAB94108
ID      AAB94108 standard; protein; 560 AA.
XX
XX      AAB94108;
XX
XX      26-JUN-2001 (first entry)
XX
XX      Human protein sequence SEQ ID NO:14340.
XX
XX      Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
XX      Homo sapiens.
XX
XX      EP1074617-A2.
XX
XX      07-FEB-2001.
XX
XX      28-JUL-2000; 2000EP-00116126.
XX
XX      29-JUL-1999; 99JP-00248036.
XX
XX      27-AUG-1999; 99JP-00300253.
```

PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
XX Claim 8; SEQ ID NO 14340; 2537pp + Sequence Listing; English.
PS
XX The present invention describes primer sets for synthesizing 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
XX Sequence 560 AA;
SQ
Query Match 65.5%; Score 1110.5; DB 4; Length 560;
Best Local Similarity 76.6%; Pred. No. 1.9e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB 258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHGAALDLSPLHRSPHPSRQAIFCWMFS 317
QY 43 VPLPLPPLAGLLVQOIIFLGTTLALFLVLMVPLHGRNLLFRSLESWPFWLTALAVI 102
DB 318 AYQTAFICGLGLVQOIIFLGTTLALFLVLMVPLHGRNLLFRSLESWPFWLTALAVI 377
QY 103 LQNAAHVWFLETHDGHQPOLTNRRVLYAATFLLPLNLVGMXXXC----- 149
DB 378 LQNAAHVWFLETHDGHQPOLTNRRVLYAATFLLPLNLVGMVATRWVLSALYNALH 437
QY 150 -SPSIAIRHP-----TPGYTYVNFLEKIEVSQSHPAMTAFCSLLIQAQSLPRTWAAPQD 203
DB 438 GQMDLSLLPPRAATLDPGYTYVNFLEKIEVSQSHPAMTAFCSLLIQAQSLPRTWAAPQD 497
QY 204 SURGEEDEGMQLLTKDSMAKGPARGARGLAYTLHNPTLQVFRKTALLGANG 263
DB 498 SURGEEDEGMQLLTKDSMAKGPARGARGLAYTLHNPTLQVFRKTALLGANG 557
QY 264 AQP 266
DB 558 AQP 560

RESULT 5

ABP69799
ID ABP69799 standard; protein; 560 AA.
XX
AC ABP69799;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1846.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
FN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
XX WPI; 2002-759812/82.
DR N-PSDB; ABZ12016.
XX
XX New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative, or platelet
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 9; SEQ ID NO 1846; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis infections (bacterial, viral, fungal, parasitic).
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 560 AA;
Query Match 65.5%; Score 1110.5; DB 5; Length 560;
Best Local Similarity 76.6%; Pred. No. 1.9e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB 258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHGAALDLSPLHRSPHPSRQAIFCWMFS 317
QY 43 VPLPLPPLAGLLVQOIIFLGTTLALFLVLMVPLHGRNLLFRSLESWPFWLTALAVI 102

Db 318 AYQTAFICGLLVQOIIIFLGTALAFVLVMPVLHGRNLLFRSLESSWPFWLTALAVI 377
 QY 103 LQNMAAHVFLETHDGHQPOLNRRVLYAATFLLFNLVVGAMXXC----- 149
 Db 378 LQNMAAHVFLETHDGHQPOLNRRVLYAATFLLFNLVVGAMVATWRVLSALYNAIHL 437
 QY 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLPRTMAAPQD 203
 Db 438 GQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLPRTMAAPQD 497
 QY 204 SLRPGEEDEGMQLQTKDSMAKARGPAGXRGARWGLAYTLHNPQLQVFRKTALLGANG 263
 Db 498 SLRPGEEDEGMQLQTKDSMAKARGPAGSRRGRWGLAYTLHNPQLQVFRKTALLGANG 557
 QY 264 AQP 266
 Db 558 AQP 560

RESULT 6
 ADB64152
 ID ADB64152 standard; protein; 599 AA.

XX ADB64152;

DT 04-DEC-2003 (first entry)

XX Human protein encoded by clone CTONG20041260.

XX Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
 KW cell regeneration; membrane protein; signal transduction-related protein;
 KW transcription-related protein; osteoporosis; neurological disease;
 KW cancer; tumour.

XX Homo sapiens.

XX EP1308459-A2.

XX 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.

XX 05-NOV-2001; 2001JP-00379298.

XX 25-JAN-2002; 2002US-00350978.

XX (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX WPI; 2003-450961/43.

DR N-PSDB; ADB62182.

XX New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.

XX Claim 1; Page; 222pp; English.

XX The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related

CC genes may be included in them, for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours). The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a protein of the invention. Note: Some of the
 CC sequence data for this patent is not represented in the printed
 CC specification, but is based on sequence information supplied by the
 CC European Patent Office.

XX Sequence 599 AA;

Query Match 65.5%; Score 1110.5; DB 7; Length 599;
 Best Local Similarity 76.6%; Pred. No. 2.1e-106;
 Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSQSGSD-----GQFSWNLFS 42
 Db 297 CYISALVLSCLLTFLVLMRSLVTHR-----LGSQSGSD-----GQFSWNLFS 356
 QY 43 VPLPLPPLAGLLVQOIIIFLGTALAFVLVMPVLHGRNLLFRSLESSWPFWLTALAVI 102
 Db 357 AYQTAFICGLLVQOIIIFLGTALAFVLVMPVLHGRNLLFRSLESSWPFWLTALAVI 416
 QY 103 LQNMAAHVFLETHDGHQPOLNRRVLYAATFLLFNLVVGAMXXC----- 149
 Db 417 LQNMAAHVFLETHDGHQPOLNRRVLYAATFLLFNLVVGAMVATWRVLSALYNAIHL 476
 QY 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLPRTMAAPQD 203
 Db 477 GQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAQSLPRTMAAPQD 536
 QY 204 SLRPGEEDEGMQLQTKDSMAKARGPAGXRGARWGLAYTLHNPQLQVFRKTALLGANG 263
 Db 537 SLRPGEEDEGMQLQTKDSMAKARGPAGSRRGRWGLAYTLHNPQLQVFRKTALLGANG 596
 QY 264 AQP 266
 Db 597 AQP 599

RESULT 7

ABU82087
 ID ABU82087 standard; protein; 666 AA.

XX ABU82087;

XX 26-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO10282.

XX Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
 KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
 KW gene therapy; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
 KW age-related macular degeneration; atherosclerosis; hypertension;
 KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
 KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
 KW liver carcinoma; wound healing; chromosome mapping; gene mapping.

XX Homo sapiens.

XX US2003088063-A1.

XX 08-MAY-2003.

XX 12-AUG-2002; 2002US-00219003.

XX 25-JUL-2000; 2000US-0220664P.

PR 01-JUN-2001; 2001WO-US017800.

```

PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KF, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-393229/37.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal.
XX
XX Claim 11; Fig 80; 314pp; English.
XX
XX The invention describes one hundred and eighty seven nucleic acids
XX encoding novel human secreted and transmembrane (PRO) polypeptides. The
XX PRO nucleic acids, polypeptides, agonists and antagonists are useful for
XX treating or diagnosing a cardiovascular, endothelial or angiogenic
XX disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
XX related macular degeneration, atherosclerosis, hypertension, arterial
XX restenosis, rheumatoid arthritis, angina, myocardial infarctions,
XX thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
XX carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
XX have applications in molecular biology, including use as hybridisation
XX probes, and in chromosome and gene mapping. This is the amino acid
XX sequence of a novel human secreted and transmembrane PRO polypeptide
XX
XX Sequence 666 AA;
XX
XX Query Match 65.5%; Score 1110.5; DB 6; Length 666;
XX Best Local Similarity 76.6%; Pred. No. 2.4e-106;
XX Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
XX
XX 1 CYISALVLSCLTFLVLMRSLVTHR-----LGSGSGD-----GQFSWNLF 42
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 364 CYISALVLSCLTFLVLMRSLVTHRNLRLHRAALDLSPLHRSPHSRQAIFCWSFS 423
XX
XX 43 VPLPPLPAGLLVQOIIIFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 424 AYQTAFICLGLVQOIIIFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 483
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 103 LQNAAHVWFLETHDGHQPLTNRRVLYAATFLFLNVLVGMVAXXC----- 149
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 484 LQNAAHVWFLETHDGHQPLTNRRVLYAATFLFLNVLVGMVATWRVLLSALYNAHL 543
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTMAAPQD 203
XX ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 544 GQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTMAAPQD 603
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 204 SLRPGEEDEGMQLLOTQDSMAKGPARGXRGARWGLAYTLHNPTLQVFRKTALLGANG 263
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 604 SLRPGEEDEGMQLLOTQDSMAKGPARGXRGARWGLAYTLHNPTLQVFRKTALLGANG 663
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX
XX 264 AQP 266
XX |||||
XX 664 AQP 666
XX
XX RESULT 8
XX AAU04557
XX ID AAU04557 standard; protein; 667 AA.
XX
XX AC AAU04557;
XX
XX 26-SEP-2001 (first entry)
XX
XX Human Stra6 homologue, PRO10282.
XX
XX Human; Stra6; PRO10282; 15q23; tumour; breast cancer; head tumour;
XX leukaemia; lymphoid malignancy; inflammatory disorder;
XX immunogenic disorder; antigen; antibody.
XX

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XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Modified-site 8..12
XX FT Region /note= "Asn is N-glycosylated"
XX FT Region /label= N_myristoylation_site
XX FT Domain 54..69
XX FT /label= Transmembrane_domain
XX FT Region 89..97
XX FT /note= "Region deleted in Stra6 variant PRO19578"
XX FT Domain 102..119
XX FT /label= Transmembrane_domain
XX FT Region 132..140
XX FT /note= "ATP/GTP-binding site motif A (P-loop)"
XX FT Domain 148..166
XX FT Region /label= Transmembrane_domain
XX FT Region 176..182
XX FT /label= N_myristoylation_site
XX FT Domain 207..222
XX FT /label= Transmembrane_domain
XX FT Region 241..247
XX FT /label= N_myristoylation_site
XX FT Domain 301..320
XX FT /label= Transmembrane_domain
XX FT Region 317..323
XX FT /label= N_myristoylation_site
XX FT Region 341..347
XX FT /label= N_myristoylation_site
XX FT Domain 364..380
XX FT /label= Transmembrane_domain
XX FT Region 364..375
XX FT /note= "Prokaryotic membrane lipoprotein attachment site"
XX FT Domain 431..451
XX FT /label= Transmembrane_domain
XX FT Domain 474..489
XX FT /label= Transmembrane_domain
XX FT Region 525..531
XX FT /label= N_myristoylation_site
XX FT Domain 560..535
XX FT /label= Transmembrane_domain
XX FT Region 627..633
XX FT /label= N_myristoylation_site
XX FT Region 631..637
XX FT /label= N_myristoylation_site
XX FT Region 640..646
XX FT /label= N_myristoylation_site
XX FT Region 661..667
XX FT /label= N_myristoylation_site
XX
XX WO200151635-A2.
XX
XX 19-JUL-2001.
XX
XX 11-JAN-2001; 2001WO-US000847.
XX
XX 13-JAN-2000; 2000US-0175849P.
XX 14-APR-2000; 2000US-0197089P.
XX 29-AUG-2000; 2000US-0228914P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Pennica D, Smith V, Wood WI;
XX
XX WPI; 2001-442146/47.
XX N-PSDB; AAS08630.
XX
XX Human nucleic acid encoding a PRO10282 or PRO19578 polypeptide (the PRO
XX polypeptides are referred to as Stra6 polypeptides), useful in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping.
XX

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Claim 24; Fig 2; 159pp; English.

The sequence is human PR010282, a homologue of murine Stra6, a retinoic acid responsive protein thought to play an important role in early dorsoventral limb patterning during development and later in the control of endochondral ossification. The gene for the Stra6 homologue is located on chromosome 15q23. The Stra6 polypeptides, agonists, antagonists or anti-Stra6 antibodies are useful for preparation of a medicament useful in the treatment of a condition which is responsive to the Stra6 polypeptides, agonists, antagonists or anti-Stra6 antibodies. The Stra6 polypeptides may also be employed as molecular weight markers for protein electrophoresis. The Stra6 nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. The antibodies and other anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of amplified genes. Exemplary conditions or disorders include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours, leukaemias and other malignancies), neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoealic disorders, CC inflammatory, angiogenic and immunogenic disorders

XX Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 4; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGGSGSGD-----GQFSNLF 42
DB 365 CYISALVLSCLLTFLVLMRSLVTHRNLRALHGAALDLSPLHSPHPSRQAIFCWMSPS 424

QY 43 VPLPPLAGLVVQIIFLGTALAFVLMPLVHGRNLLFPRSLSSPFWLTALAVI 102
DB 425 AVQTAFICLGLVQIIFLGTALAFVLMPLVHGRNLLFPRSLSSPFWLTALAVI 484

QY 103 LQMAAHWFLETHDGHQPQTNRRVLYAATFLFPLNLVGMATVTRVLLSALYNAIHL 149
DB 485 LQMAAHWFLETHDGHQPQTNRRVLYAATFLFPLNLVGMATVTRVLLSALYNAIHL 544

QY 150 -SPSIAIRHP-----TFGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAPOD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAPOD 604

QY 204 SLRPGDEEGMQLQTKDSMAKGRFCAKGRARWGLAYTLHNPTLQVFRKTLGANG 263
DB 605 SLRPGDEEGMQLQTKDSMAKGRFCAKGRARWGLAYTLHNPTLQVFRKTLGANG 664

QY 264 AQP 266
DB 665 AQP 667

RESULT 9

AA888572
ID AAB88572 standard; protein; 667 AA.

XX AAB88572;

XX 04-JUN-2001 (first entry)

DE Human hydrophobic domain containing protein clone HP10713 #36.

XX Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
XX antianaemic; vulnary; antiulcer; osteopathic; anti-inflammatory;
XX cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW behavioural characteristic; immune response.

XX Homo sapiens.

XX WO200112660-A2.
XX 22-FEB-2001.
XX 10-AUG-2000; 2000WO-JP0053356.
XX 17-AUG-1999; 99JP-00230344.
XX 07-SEP-1999; 99JP-00252551.
XX 01-OCT-1999; 99JP-00281132.
XX 22-OCT-1999; 99JP-00301624.
XX 04-NOV-1999; 99JP-00313877.
XX (SAGA) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.
XX Kato S, Kimura T;
XX WPI; 2001-160059/16.
XX N-PSDB; AAF94442.
XX Human proteins with hydrophobic domains and the DNAs which encode them
XX are useful for treating autoimmune disorders, burns and tumors and for
XX screening novel pharmaceuticals.
XX Claim 1; Page 288-291; 518pp; English.
XX AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
XX AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
XX anti-HIV, neuroprotective, antianaemic, vulnary, antiulcer,
XX osteopathic, anti-inflammatory and cytostatic activities, and can be used
XX in gene therapy. (I) can be used as pharmaceuticals and as antigens to
XX prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
XX for genetic diagnosis and gene sources for gene therapy or for producing
XX (I) in large quantities. Cells containing (II) are used for the detection
XX of ligands or receptors corresponding to membrane or secretory proteins
XX and to screen small molecule novel pharmaceuticals. Antibodies directed
XX to (I) can be used for the detection, quantification and purification of
XX (I). Activities of (I) may include cytokine and cell
XX proliferation/differentiation function, immune stimulating or suppressing
XX activity, haematopoiesis regulating activity, tissue growth activity,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity and anti-inflammatory
XX activity. (I) and (II) can be used to treat autoimmune disorders e.g.
XX multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
XX inflammatory bowel disease and tumours. (I) and (II) can also be used for
XX wound healing, as nutritional sources or supplements e.g. as amino acid,
XX carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
XX processing and utilisation of dietary fat, protein, carbohydrate,
XX vitamins and minerals, to effect behavioural characteristics, to affect
XX appetite, and can act as antigens in vaccines to raise an immune response
XX to the protein or another material cross-reactive with the protein
XX Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 4; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGGSGSGD-----GQFSNLF 42
DB 365 CYISALVLSCLLTFLVLMRSLVTHRNLRALHGAALDLSPLHSPHPSRQAIFCWMSPS 424

QY 43 VPLPPLAGLVVQIIFLGTALAFVLMPLVHGRNLLFPRSLSSPFWLTALAVI 102
DB 425 AVQTAFICLGLVQIIFLGTALAFVLMPLVHGRNLLFPRSLSSPFWLTALAVI 484

QY 103 LQMAAHWFLETHDGHQPQTNRRVLYAATFLFPLNLVGMATVTRVLLSALYNAIHL 149
DB 485 LQMAAHWFLETHDGHQPQTNRRVLYAATFLFPLNLVGMATVTRVLLSALYNAIHL 544

QY 150 -SPSIAIRHP-----TFGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAPOD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAPOD 604

QY 204 SLRPGDEEGMQLQTKDSMAKGRFCAKGRARWGLAYTLHNPTLQVFRKTLGANG 263
DB 605 SLRPGDEEGMQLQTKDSMAKGRFCAKGRARWGLAYTLHNPTLQVFRKTLGANG 664

QY 264 AQP 266
DB 665 AQP 667

Db 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPMATFACSLLIQAQSLLPRTMAAPQD 604
QY 204 SLRPGEEDEGMQLLQTKDSMAKGPAGXRGARWGLAYTLHNPFTLQVFRKTLGANG 263
Db 605 SLRPGEEDEGMQLLQTKDSMAKGPAGXRGARWGLAYTLHNPFTLQVFRKTLGANG 664
QY 264 AQP 266
Db 665 AQP 667
RESULT 10
AAU83631
ID AAU83631 standard; protein; 667 AA.
AC AAU83631;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 80.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
WPI; 2002-172001/22.
DR N-PSDB; ABK33575.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX

PS Claim 11; Fig 80; 359bp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 667 AA;
Query Match 65.5%; Score 1110.5; DB 5; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGSGD-----GQFSWNLFS 42
Db 365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRAALDLSPLHRSPPHPSRAIFCWMSFS 424
QY 43 VPFLPPLAGLLVQOIIFFLGTTALAFVLMPVLHGRNLLFFRSLESWPFWLTALAVI 102
Db 425 AYQTAFICGLLVQOIIFFLGTTALAFVLMPVLHGRNLLFFRSLESWPFWLTALAVI 484
QY 103 LQNAAHWVFLTHDGHPLTNRRVLYAATFLPLVNLVGMATVRLVLSALYNAHL 544
Db 485 LQNAAHWVFLTHDGHPLTNRRVLYAATFLPLVNLVGMATVRLVLSALYNAHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPMATFACSLLIQAQSLLPRTMAAPQD 203
Db 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPMATFACSLLIQAQSLLPRTMAAPQD 604
QY 204 SLRPGEEDEGMQLLQTKDSMAKGPAGXRGARWGLAYTLHNPFTLQVFRKTLGANG 263
Db 605 SLRPGEEDEGMQLLQTKDSMAKGPAGXRGARWGLAYTLHNPFTLQVFRKTLGANG 664
QY 264 AQP 266
Db 665 AQP 667
RESULT 11
AAU78575
ID AAU78575 standard; protein; 667 AA.
XX
AC AAU78575;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Stra6 (PRO10282) protein.
XX
KW Human; cancer; Stra6; PRO10282; cytostatic; stromal disorder; tumour;
KW retinoid; Wnt; tumour antigen; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; blastococelic disorder; chromosome 15q23.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 8..12 /note= "N Glycosylation site"
FT Region 50..56 /note= "N-myristoylation site"
FT

XX PD 29-NOV-2001.
 XX PF 24-MAY-2001; 2001WO-US017073.
 XX 24-MAY-2000; 2000US-0206679P.
 PR 24-MAY-2000; 2000US-0206688P.
 PR 24-MAY-2000; 2000US-0206829P.
 PR 30-MAY-2000; 2000US-0207748P.
 PR 30-MAY-2000; 2000US-0207798P.
 PR 31-MAY-2000; 2000US-0208263P.
 PR 02-JUN-2000; 2000US-0208831P.
 PR 05-JUN-2000; 2000US-0209451P.
 PR 07-JUN-2000; 2000US-0210060P.
 PR 20-JUL-2000; 2000US-0219507P.
 PR 26-JUL-2000; 2000US-0221337P.
 PR 31-JUL-2000; 2000US-0221927P.
 PR 19-JAN-2001; 2001US-0263135P.
 PR 24-JAN-2001; 2001US-0263688P.
 PR 24-JAN-2001; 2001US-0263694P.
 PR 23-MAY-2001; 2001US-00863776.
 XX (CURA-) CURAGEN CORP.
 XX Spytek KA, Majumder K, Tchernev VT, Mishra V, Padigaru M;
 PI Spaderna SK, Shenoy S, Rastelli L, Li L, Taupier RJ, Gangolli E;
 XX WPI; 2002-106174/14.
 DR N-PSDB; ABA92669.
 XX Novel polypeptide, useful for treating pain, cancer, urinary retention,
 PT osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
 PT asthma, ulcer, allergy and Huntington's disease, comprises isolated
 PT polypeptide NOVX.
 XX Claim 1; Page 106; 266pp; English.
 PS The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
 CC proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
 CC fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
 CC antiasthmatic, hypotensive, osteopathic, antiinflammatory, antitumor,
 CC neuroprotective, cardiac, antiallergic, antidepressant, nootropic,
 CC anticonvulsant and neuroleptic activities. (I) and polynucleotides (II)
 CC can be used in gene therapy and vaccine production. (I) and (II) can be
 CC used for treating or preventing a NOVX-associated disorder such as
 CC cardiomyopathy, atherosclerosis and diabetes in a human, where the
 CC disorder is related to cell signal processing and metabolic path way
 CC modulation, in a subject, preferably human. (I) and (II) can be used for
 CC diagnosing, preventing or treating developmental diseases, immune
 CC diseases, taste and scent detectability disorder, Burkitt's lymphoma,
 CC signal transduction pathway disorders, retinal diseases including those
 CC involving photoreception, cell growth rate disorders, feeding disorders,
 CC noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
 CC Parkinson's disease, acute heart failure, hypotension, hypertension,
 CC urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
 CC Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
 CC infarction, allergies, benign prostatic hypertrophy, manic depression,
 CC delirium, dementia, severe metal retardation and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome. The present
 CC sequence represents the human NOVXc protein from the present invention.
 CC Human NOV2a is isolated to chromosome 15
 XX
 SQ Sequence 667 AA;
 Query Match 65.5%; Score 1110.5; DB 5; Length 667;
 Best Local Similarity 76.6%; Pred. No. 2.4e-106;
 Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
 QY 1 CVISALVLSCLTFLVLRSLVTHR-----LGSGGSGP-----GQESWNLF 42
 DB 365 CVISALVLSCLTFLVLRSLVTHRTNLRHGAALDLSPLRSPHPSRQAFQWGF 424
 QY 43 VPLPLPLAGLVQOIIFFLGTALAFVLMVPLHGRNLLFFRSLESSPFWLTLALAVI 102

Db 425 AYQTAFICGLLVQOIIFFLGTALAFVLMVPLHGRNLLFFRSLESSPFWLTLALAVI 484
 QY 103 LQNMAAHWVFLTEHDGHPQLNRRVLYAATFLLPPLNVLGAMXXC----- 149
 Db 485 LQNMAAHWVFLTEHDGHPQLNRRVLYAATFLLPPLNVLGAMVATWVLLSALYNAIHL 544
 QY 150 -SPSIATRHP-----TCGYTYRNFLKIEVSQSHPMATFACSLLLQAOSLLPRTMAAPQD 203
 Db 545 GOMDSLPLPPRAAFLDPGYTYRNFLKIEVSQSHPMATFACSLLLQAOSLLPRTMAAPQD 604
 QY 204 SLRPGEEDEGNQLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTLALGANG 263
 Db 605 SLRPGEEDEGNQLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTLALGANG 664
 QY 264 AQP 266
 Db 665 AQP 667

RESULT 13
 AA019413
 ID AA019413 standard; protein; 667 AA.
 AC AA019413;
 XX 10-DEC-2002 (first entry)
 DT Human molecule for disease detection and treatment protein #16.
 XX Human; molecule for disease detection and treatment; MDDT; gene therapy;
 KW cytostatic; antiarteriosclerotic; hepatotropic; anti-HIV; antiallergic;
 KW antiinflammatory; antiasthmatic; cerebroprotective; nootropic;
 KW neuroprotective; antiparkinsonian; cardiant; antianginal.
 XX Homo sapiens.
 OS WO200270709-A2.
 PN 12-SEP-2002.
 PD 08-FEB-2002; 2002WO-US003709.
 PR 09-FEB-2001; 2001US-0268117P.
 PR 15-FEB-2001; 2001US-0269618P.
 PR 23-FEB-2001; 2001US-0271118P.
 PR 07-MAR-2001; 2001US-0274486P.
 PR 09-MAR-2001; 2001US-0274436P.
 PR 28-NOV-2001; 2001US-0334229P.
 PR 01-FEB-2002; 2002US-0353284P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Lal PG, Baughn MR, Yao MG, Walia NK, Elliot VS, Xu Y;
 XX Honchell CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DAM;
 PI Hafalia AJA, Ghandi AR, Thangavelu K, Sanjanwala MM, Tang YT;
 PI Rankumar J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein SK;
 PI Burford N, Lee EA, Lu Y, Iran UK, Marquis JP;
 XX WPI; 2002-713453/77.
 DR N-PSDB; AAL49942.
 XX New human molecules for disease detection and treatment (MDDT), useful
 PT for diagnosing, treating and preventing diseases or conditions associated,
 PT with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
 PT hepatitis.
 XX Claim 1; Page 148-150; 177pp; English.
 PS The present invention relates to human proteins and coding sequences of
 CC molecules for disease detection and treatment MDDT. The sequences can be
 CC used in the treatment of diseases associated with the decreased
 CC expression or overexpression of MDDT, such as cell proliferative (cancer,

CC atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS, CC allergies, Addison's disease, asthma), developmental (dwarfism, renal CC tubular acidosis), neurological (e.g. stroke, Parkinson's disease, CC epilepsy) and cardiovascular (congestive heart failure, myocardial CC infarction, angina pectoris) disorders. The present sequence is a protein CC of the invention

XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 5; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYSALVLSCLTFLVLMRSLVTHR-----LGGSGSD-----GQFSWNLFS 42
DB 365 CYSALVLSCLTFLVLMRSLVTHRNLRLHRAALDLSPLHRSPHRSQAIFCWSFS 424

QY 43 VPLPLPPLAGLVQIIFELGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLALAVI 102
DB 425 AYQTAFICGLLVQIIFELGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLALAVI 484

QY 103 LQMAAHWVLETHDGHQPQTNRRVLYAATFLLPLNLVGMATVRLLSALYNAIHL 149
DB 485 LQMAAHWVLETHDGHQPQTNRRVLYAATFLLPLNLVGMATVRLLSALYNAIHL 544

QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLLPPRAATLDPGYTYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604

QY 204 SLRPGEEDEGMQLLOTKDSMAKARGPAGXRGARWGLAYTLNHNPTLQVFRKTALLGANG 263
DB 605 SLRPGEEDEGMQLLOTKDSMAKARGPAGXRGARWGLAYTLNHNPTLQVFRKTALLGANG 664

QY 264 AQP 266
DB 665 AQP 667

RESULT 14
ABU80778
ID ABU80778 standard; protein; 667 AA.
AC ABU80778;
XX
DT 23-JUN-2003 (first entry)
XX Human PRO polypeptide #40.
XX Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX Homo sapiens.
XX US2003036635-A1.
XX 20-FEB-2003.
XX 28-AUG-2002; 2002US-00230163.
XX 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-342045/32.
DR N-PSDB; ACA66880.
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT

PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
XX Claim 11; Fig 80; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing antibodies
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80733-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/paipsdIDentry.html

XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 6; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYSALVLSCLTFLVLMRSLVTHR-----LGGSGSD-----GQFSWNLFS 42
DB 365 CYSALVLSCLTFLVLMRSLVTHRNLRLHRAALDLSPLHRSPHRSQAIFCWSFS 424

QY 43 VPLPLPPLAGLVQIIFELGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLALAVI 102
DB 425 AYQTAFICGLLVQIIFELGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLALAVI 484

QY 103 LQMAAHWVLETHDGHQPQTNRRVLYAATFLLPLNLVGMATVRLLSALYNAIHL 149
DB 485 LQMAAHWVLETHDGHQPQTNRRVLYAATFLLPLNLVGMATVRLLSALYNAIHL 544

QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLLPPRAATLDPGYTYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604

QY 204 SLRPGEEDEGMQLLOTKDSMAKARGPAGXRGARWGLAYTLNHNPTLQVFRKTALLGANG 263
DB 605 SLRPGEEDEGMQLLOTKDSMAKARGPAGXRGARWGLAYTLNHNPTLQVFRKTALLGANG 664

QY 264 AQP 266
DB 665 AQP 667

RESULT 15
ABO33744
ID ABO33744 standard; protein; 667 AA.
XX ABO33744;
XX
DT 17-SEP-2003 (first entry)
XX Novel human secreted and transmembrane protein PRO10282.
XX Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioresactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX Homo sapiens.
XX US2003045687-A1.
XX 06-MAR-2003.
XX 12-AUG-2002; 2002US-00218631.
PF

XX 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX (GETH) GENENTECH INC.
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-512315/48.
DR N-PSDB; ACD68632.
XX New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating tumor necrosis factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX Claim 11; Fig 80; 314pp; English.
XX The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumors (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumors or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
XX Sequence 667 AA;
Query Match 65.5%; Score 1110.5; DB 6; Length 667;
Best Local Similarity 76.6%; Pred No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLTFVLVRLSVLTHR-----LGSGGSGD-----GQFSWNLFS 42
Db 365 CYISALVLSCLLTFVLVRLSVLTHRLRALHGAALDPLHRSRQAIFCWMSFS 424
QY 43 VPLPPLPGLAGLLVQIIIFLGTALAFVLMVPLHGRNLLFRSLSSWPPWLTALAVI 102
Db 425 AYQTAFICLGLLVQIIIFLGTALAFVLMVPLHGRNLLFRSLSSWPPWLTALAVI 484
QY 103 LQNMAAHWVFLTHDGHQPOLNRRVLYAATFLFLNVLVGMXXC----- 149
Db 485 LQNMAAHWVFLTHDGHQPOLNRRVLYAATFLFLNVLVGMVATWRLVLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYTNRNFKIEVSQSHPAMTAFCSLLIQAOSLLPRTMAAPQD 203
Db 545 GQMDLSLLPPRAATLDPGYTYTNRNFKIEVSQSHPAMTAFCSLLIQAOSLLPRTMAAPQD 604
QY 204 SLRPGEEDEGMQLLOTKDSMAKGPARGARGLAYTLHNPQLQVFRKTLALIGANG 263
Db 605 SLRPGEEDEGMQLLOTKDSMAKGPARGARGLAYTLHNPQLQVFRKTLALIGANG 664
QY 264 AQP 266

Db 665 AQP 667
Search completed: February 8, 2005, 13:36:13
Job time : 146.513 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:30:00 ; Search time 38.4542 Seconds
(without alignments)
630.905 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYSALVSLTLFLVLMRS.....APPTWLWESQGFWRKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	440	26.0	88	4	US-09-205-258-274
2	98.5	5.8	157	4	US-09-252-991A-30836
3	94.5	5.6	726	4	US-09-252-991A-18271
4	93.5	5.5	422	4	US-09-252-991A-19452
5	93	5.5	2016	3	US-09-634-320-4
6	93	5.5	2016	4	US-09-514-907A-2
7	93	5.5	2016	4	US-09-896-994-2
8	93	5.5	2016	4	US-09-840-125-4
9	92	5.4	1272	4	US-09-949-016-7472
10	92	5.4	2146	4	US-09-949-016-6947
11	90.5	5.3	557	4	US-09-902-540-12884
12	90.5	5.3	1241	4	US-08-714-741-34
13	90	5.3	327	4	US-09-252-991A-29468
14	89.5	5.3	275	4	US-09-252-991A-16752
15	89.5	5.3	434	4	US-09-252-991A-30855
16	89	5.3	249	4	US-09-602-777A-344
17	88.5	5.2	501	4	US-09-252-991A-32497
18	87	5.1	618	3	US-08-866-381A-6
19	87	5.1	621	1	US-08-208-887A-49
20	87	5.1	621	3	US-09-280-598-18
21	87	5.1	621	4	US-08-945-771-4
22	86.5	5.1	465	4	US-09-456-239A-18
23	86	5.1	597	4	US-09-252-991A-24252
24	85.5	5.0	395	4	US-09-489-039A-12123
25	85	5.0	809	4	US-09-252-991A-12123
26	84.5	5.0	299	4	US-09-393-634-41
27	84.5	5.0	738	4	US-09-949-016-10957

28	84	5.0	484	4	US-09-252-991A-32299
29	84	5.0	529	4	US-09-489-039A-7581
30	84	5.0	595	4	US-09-252-991A-17434
31	84	5.0	1395	4	US-09-949-016-7109
32	83.5	4.9	922	4	US-09-569-611C-41
33	83.5	4.9	971	4	US-09-868-572A-1
34	83	4.9	526	4	US-09-438-185A-37
35	83	4.9	539	3	US-09-036-987A-11
36	83	4.9	539	3	US-09-370-700-11
37	83	4.9	539	4	US-09-603-207-11
38	83	4.9	1122	4	US-09-252-991A-22843
39	83	4.9	1495	3	US-08-462-467B-12
40	82.5	4.9	216	4	US-09-134-000C-4728
41	82.5	4.9	344	4	US-09-252-991A-24536
42	82.5	4.9	1024	4	US-09-562-737-84
43	82.5	4.9	2972	4	US-08-469-260A-387
44	82.5	4.9	2972	4	US-08-488-446-387
45	82.5	4.9	2372	4	US-08-467-344A-387

ALIGNMENTS

RESULT 1
US-09-205-258-274
; Sequence 274, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

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; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 274
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-274
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Query Match          26.0%; Score 440; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.3e-39; Indels 0; Gaps 0;
Matches 87; Conservative 0; Mismatches 0;

QY 180 MTAFCSLLLQAQSLLPRTMAAPQDSLRPGCEDEGMLLOTKDSMAKGARPGAXRGRARWG 239
DB 1 MTAFCSLLLQAQSLLPRTMAAPQDSLRPGCEDEGMLLOTKDSMAKGARPGAXRGRARWG 60

QY 240 LAYTLHNPTLQVFRKLTALLGANGAQP 266
DB 61 LAYTLHNPTLQVFRKLTALLGANGAQP 87
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RESULT 2
US-09-252-991A-30836
; Sequence 30836, Application US/09252991A
; Patent No. 6551795
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```
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30836
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30836
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Query Match          5.8%; Score 98.5; DB 4; Length 157;
Best Local Similarity 33.0%; Pred. No. 0.015;
Matches 30; Conservative 6; Mismatches 26; Indels 29; Gaps 3;
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QY 195 PRTMAAPQDSLRPGCEDEGMLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPTLQVFR 254
DB 2 PAARRGCRDRARP-----RPRSPAPGARPGARRGRHSTA----- 38
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```
QY 255 KTALLGANGAQCSSL--PGSPPSITPAMQP 283
DB 39 ----TGRRRPARPAATLAGPGSPGCRPAAI 65
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RESULT 3

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US-09-252-991A-18271
; Sequence 18271, Application US/09252991A
; Patent No. 6551795
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GENERAL INFORMATION:

```
; APPLICANT: Marc J. Rubenfield et al.
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

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; FILE REFERENCE: 107196.136
```

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; CURRENT APPLICATION NUMBER: US/09/252,991A
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; CURRENT FILING DATE: 1999-02-18
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; PRIOR APPLICATION NUMBER: US 60/074,788
```

```
; PRIOR FILING DATE: 1998-02-18
```

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; PRIOR APPLICATION NUMBER: US 60/094,190
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```
; PRIOR FILING DATE: 1998-07-27
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; NUMBER OF SEQ ID NOS: 33142
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; SEQ ID NO 18271
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; LENGTH: 726
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; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-18271
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Query Match          5.6%; Score 94.5; DB 4; Length 726;
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Best Local Similarity 31.7%; Pred. No. 0.31;
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Matches 33; Conservative 10; Mismatches 44; Indels 17; Gaps 5;
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QY 194 LPR--TMAAPQDSLRPGCEDEG--MQLLOTKDSMAKGARPGAXRGRARWGLAYTLHNPT 249
DB 273 LPRGCTAVLHNDPGRPGDPGDRLLLPDPQAQDQHPGDPHGRG--GRRFP----- 324
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QY 250 LQVFRKLTALLGANGAQCSSLPGSPPSITPAMQAPGPDHGXV 293
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```
DB 325 ---RRVFLLPRLAGLQPGQLPERQPL-PRLLDGPWPAVHQGPV 363
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RESULT 4

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US-09-252-991A-19452
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; Sequence 19452, Application US/09252991A
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```
; Patent No. 6551795
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GENERAL INFORMATION:

```
; APPLICANT: Marc J. Rubenfield et al.
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A

;; CURRENT FILING DATE: 1999-02-18

;; PRIOR APPLICATION NUMBER: US 60/074,788

;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190

;; PRIOR FILING DATE: 1998-07-27

;; NUMBER OF SEQ ID NOS: 33142

;; SEQ ID NO 19452

;; LENGTH: 422

;; TYPE: PRT

;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19452

Query Match 5.5%; Score 93.5; DB 4; Length 422;

Best Local Similarity 23.8%; Pred. No. 0.19; Indels 73; Gaps 10;

Matches 48; Conservative 14; Mismatches 73; Indels 73; Gaps 10;

QY 135 LPLNLVGMXXKCSPSIAIRHPTPGYTYRNFLEKIEVSQSHP-AMTAFCSLLLQAQSL 193

DB 129 LPLGCFVPLVSLCHRLRNAPRSG-----QTAPDSQAFLSL---RYSL 172

QY 194 LPTMAAPQDSLRPGDEEGMQLQTKDSMAKGARPCAXRG-----RAR 237

DB 173 ALKISATP-----GVDEYKTR---KGNMSGPLRGVFLTPCTPAPRKLVTSSRG 217

QY 238 WGLAYTLHNPTLOVFRKTKALLGANGAQCSSLPGSPSITPAMQAGPDHGXVEVCL 297

DB 218 NGNAY---HOSHISHTASS-----HHLPGGAPCLTPSSTPAVSPTTIGSCTGCC 264

QY 298 HWEPXXGSAPPTWLWESQQGF 319

DB 265 -WNRKAGSCSPTW-----YGCW 280

RESULT 5

US-09-634-920-4

;; Sequence 4, Application US/09634920

;; Patent No. 6342357

;; GENERAL INFORMATION:

;; APPLICANT: Splawski, Igor

;; APPLICANT: Keating, Mark T.

;; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND

;; TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME

;; FILE REFERENCE: 2323-155

;; CURRENT APPLICATION NUMBER: US/09/634,920

;; CURRENT FILING DATE: 2000-08-09

;; PRIOR APPLICATION NUMBER: 60/190,057

;; PRIOR FILING DATE: 2000-03-17

;; PRIOR APPLICATION NUMBER: 60/147,488

;; PRIOR FILING DATE: 1999-08-09

;; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: PatentIn Ver. 2.0

;; SEQ ID NO 4

;; LENGTH: 2016

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-634-920-4

Query Match

Best Local Similarity 5.5%; Score 93; DB 3; Length 2016;

Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSNLFVPLPLPPLAGLVQIIFFLGTTALAFVLMPLVHGRNLLPFRSLESSWPF 94

DB 778 QCGWNIFD-----SIIVLSLMELGLSRMSNL---SVLSRFRLLRVFKLAKSWPTL 825

QY 95 -----LTLALAVILQNMMAHWV-----FLETHDGHQPOLTNR---RVLY 129

DB 826 NTLIKIIGNSVGALGNLTLLAIIVFIVAVGMQLFGKNYSELRSDSGLLRHWMDDFF 885

QY 130 AATFLLPPLNLVGMXXKCSPSIAIRHPTPGYTYRNFLEKIEVSQSHPAMTAFCSLLQ 189

DB 190 AQSLLPRTMAAPQDSLRPGDEEGMQLQTKDSMAKGARPCAXRGARWGLATLTL-HNP 248

DB 886 HAFLLIF--RILGGEWIEIETMDCMEVSGS---LCLLVFLVVMVIGNLVVLNLFALLLS 940

QY 190 AQSLLPRTMAAPQDSLRPGDEEGMQLQTKDSMAKGARPCAXRGARWGLATLTL-HNP 248

DB 941 SFS-----ADNLTAPDEDEWNNLQ---ALARIQRLFRVKTWDFCCGGLLRHRP 989

QY 249 TLQVFRKTKALLGANGAQP-CSSLPGSPSITPAMQAGPPD 288

DB 990 -----QKPAALAAQGLPSCIATPYSP-----PPE 1015

RESULT 6

US-09-514-907A-2

;; Sequence 2, Application US/09514907A

;; Patent No. 6567705

;; GENERAL INFORMATION:

;; APPLICANT: Kenneth B. Stokes

;; APPLICANT: Jose Morissette

;; TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL

;; SENSING BY CARDIAC PACEMAKERS THROUGH

;; GENETIC TREATMENT

;; NUMBER OF SEQUENCES: 12

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705ris LLP

;; STREET: One Liberty Place - 46th Floor

;; CITY: Philadelphia

;; STATE: PA

;; COUNTRY: U.S.A.

;; ZIP: 19103

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: WordPerfect 6.1

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/514,907A

;; FILING DATE: 08-Feb-2000

;; CLASSIFICATION: <Unknown>

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Paul K. Legaard

;; REGISTRATION NUMBER: 38,534

;; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (215) 568-3100

;; TELEFAX: (215) 568-3439

;; INFORMATION FOR SEQ ID NO: 2:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 2016 amino acids

;; TYPE: amino acid

;; STRANDEDNESS: single

;; TOPOLOGY: unknown

;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-514-907A-2

Query Match

Best Local Similarity 5.5%; Score 93; DB 4; Length 2016;

Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSNLFVPLPLPPLAGLVQIIFFLGTTALAFVLMPLVHGRNLLPFRSLESSWPF 94

DB 778 QCGWNIFD-----SIIVLSLMELGLSRMSNL---SVLSRFRLLRVFKLAKSWPTL 825

QY 95 -----LTLALAVILQNMMAHWV-----FLETHDGHQPOLTNR---RVLY 129

DB 826 NTLIKIIGNSVGALGNLTLLAIIVFIVAVGMQLFGKNYSELRSDSGLLRHWMDDFF 885

QY 130 AATFLLPPLNLVGMXXKCSPSIAIRHPTPGYTYRNFLEKIEVSQSHPAMTAFCSLLQ 189

DB 886 HAFLLIF--RILGGEWIEIETMDCMEVSGS---LCLLVFLVVMVIGNLVVLNLFALLLS 940

QY 190 AQSLLPRTMAAPQDSLRPGDEEGMQLQTKDSMAKGARPCAXRGARWGLATLTL-HNP 248

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Db 941 SFS-----ADNLTPADEDEMNNLQ--ALARIQGLRFVVKRTTWDFFCGLLRHP 989
QY 249 TLQVFRKRTALLGANGAQP-CSSLPGSPSITPAMQAGPPD 288
Db 990 -----QKPAALAAQQLPSCIATPYSP-----PPE 1015

RESULT 7
US-09-896-994-2
; Sequence 2, Application US/09896994
; Patent No. 6665563
; GENERAL INFORMATION:
; APPLICANT: Ken Stokes
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/896,994
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/514,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2016 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

Query Match 5.5%; Score 93; DB 4; Length 2016;
Best Local Similarity 23.8%; Pred. No. 1.8;
Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSWNLFSPVLPPLPPLAGLLVQOIIFPLGTALAFVLMPVLHGRNLLFFRSLESSWPF 94
Db 778 QQGNIFD-----SIIVLSMELGLSRMSNL---SVLRSPFLRVFKLAKSWPTL 825
QY 95 -----LTLALAVILQNMAAHWV-----FLETHDGHQPOLTNR---RVLY 129
Db 826 NTLIKIIGNSVGALGNLTVLAIIVFIFAVVGMQLFGKNYSELSDSDGSLPRWHMDDFF 885
QY 130 AATFLPLNVLVGAMXXXCSPSIAIRHPTPGYTYRNFLKIEVSQSHPAMTAFCSLLQ 189
Db 886 HAFLLIIF--RILCGEWIETWDCMEVSGQS---LCLLVFLVVMVGNLVNLFALLLS 940
QY 190 AQSLLPRTMAAPQDSLPGCEDEGMQLLOTKDSMAKGARPGAXRGARWGLAYTLL--HNP 248
Db 941 SFS-----ADNLTPADEDEMNNLQ--ALARIQGLRFVVKRTTWDFFCGLLRHP 989
QY 249 TLQVFRKRTALLGANGAQP-CSSLPGSPSITPAMQAGPPD 288

US-09-896-994-2

Query Match 5.5%; Score 93; DB 4; Length 2016;
Best Local Similarity 23.8%; Pred. No. 1.8;
Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSWNLFSPVLPPLPPLAGLLVQOIIFPLGTALAFVLMPVLHGRNLLFFRSLESSWPF 94
Db 778 QQGNIFD-----SIIVLSMELGLSRMSNL---SVLRSPFLRVFKLAKSWPTL 825
QY 95 -----LTLALAVILQNMAAHWV-----FLETHDGHQPOLTNR---RVLY 129
Db 826 NTLIKIIGNSVGALGNLTVLAIIVFIFAVVGMQLFGKNYSELSDSDGSLPRWHMDDFF 885
QY 130 AATFLPLNVLVGAMXXXCSPSIAIRHPTPGYTYRNFLKIEVSQSHPAMTAFCSLLQ 189
Db 886 HAFLLIIF--RILCGEWIETWDCMEVSGQS---LCLLVFLVVMVGNLVNLFALLLS 940
QY 190 AQSLLPRTMAAPQDSLPGCEDEGMQLLOTKDSMAKGARPGAXRGARWGLAYTLL--HNP 248
Db 941 SFS-----ADNLTPADEDEMNNLQ--ALARIQGLRFVVKRTTWDFFCGLLRHP 989
QY 249 TLQVFRKRTALLGANGAQP-CSSLPGSPSITPAMQAGPPD 288
```

```
Db 990 -----QKPAALAAQQLPSCIATPYSP-----PPE 1015

RESULT 8
US-09-840-125-4
; Sequence 4, Application US/09840125
; Patent No. 6787309
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING SAME
; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/840,125
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/634,920
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2016
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-125-4

Query Match 5.5%; Score 93; DB 4; Length 2016;
Best Local Similarity 23.8%; Pred. No. 1.8;
Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSWNLFSPVLPPLPPLAGLLVQOIIFPLGTALAFVLMPVLHGRNLLFFRSLESSWPF 94
Db 778 QQGNIFD-----SIIVLSMELGLSRMSNL---SVLRSPFLRVFKLAKSWPTL 825
QY 95 -----LTLALAVILQNMAAHWV-----FLETHDGHQPOLTNR---RVLY 129
Db 826 NTLIKIIGNSVGALGNLTVLAIIVFIFAVVGMQLFGKNYSELSDSDGSLPRWHMDDFF 885
QY 130 AATFLPLNVLVGAMXXXCSPSIAIRHPTPGYTYRNFLKIEVSQSHPAMTAFCSLLQ 189
Db 886 HAFLLIIF--RILCGEWIETWDCMEVSGQS---LCLLVFLVVMVGNLVNLFALLLS 940
QY 190 AQSLLPRTMAAPQDSLPGCEDEGMQLLOTKDSMAKGARPGAXRGARWGLAYTLL--HNP 248
Db 941 SFS-----ADNLTPADEDEMNNLQ--ALARIQGLRFVVKRTTWDFFCGLLRHP 989
QY 249 TLQVFRKRTALLGANGAQP-CSSLPGSPSITPAMQAGPPD 288
Db 990 -----QKPAALAAQQLPSCIATPYSP-----PPE 1015

RESULT 9
US-09-949-016-7472
; Sequence 7472, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7472
```

```
; LENGTH: 1272
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7472

Query Match      5.4%; Score 92; DB 4; Length 1272;
Best Local Similarity 25.3%; Pred. No. 1.2;
Matches 80; Conservative 48; Mismatches 126; Indels 62; Gaps 17;

QY 3 ISALVLSCL---LTF-----LVLMRSLVT---HRLGSGSGD-----CQFSWNL--FSV 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 660 VDVLVSICVVFAMSFVPASFTLVLEERVTRAKHLQMLGSLPTLYWLNFLWDMCNLYV 719
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 PLPLPPLAGLVQOIIFFLGTALAFVLMPLVHGRNLL-----FFRSLESSWPFWLT 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 720 PACIVVLIIFLAFOORA-YVAPANLPALLLLLLLYGWSITPLMYPASFFSVSTAYVLT 778
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 -LALAVILQNMAAHWVLETHDGHQPOLTNRRLVLYAATFLPLNLV-VGAMXXXCSPSTA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 779 CINLFIGINGSMATFVLELFSQKLOEVSRL-ILKQVFLIFPHFCLGRGLIDMVRNQAWA 836
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 IRHPTPGYTYRNFLEKIEVSQSH-----PAMTAFCSLLQAQSL---PRTMAAPQD 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 DAFERLGDROFQSPLEWVGKLLAMVIQGPLFLF-TLLQHRSQLLPQPRVSLP-- 893
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 SLRPGDEEGMQLQTKDSMAKARGP-----AXRGRARWGLAYTLHNPLOVF 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 894 --LLGEDE--DVARERERVQATQGDVLRNLTKYRGQRMAMPADVRLCIGIPGECF 949
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 254 RKTALLGANGAQCPS 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 950 ---GLLVNGAGKTST 962
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-09-949-016-6947
; Sequence 6947, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6947
; LENGTH: 2146
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6947

Query Match      5.4%; Score 92; DB 4; Length 2146;
Best Local Similarity 25.3%; Pred. No. 2.5;
Matches 80; Conservative 48; Mismatches 126; Indels 62; Gaps 17;

QY 3 ISALVLSCL---LTF-----LVLMRSLVT---HRLGSGSGD-----CQFSWNL--FSV 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1534 VDVLVSICVVFAMSFVPASFTLVLEERVTRAKHLQMLGSLPTLYWLNFLWDMCNLYV 1593
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 PLPLPPLAGLVQOIIFFLGTALAFVLMPLVHGRNLL-----FFRSLESSWPFWLT 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1594 PACIVVLIIFLAFOORA-YVAPANLPALLLLLLLYGWSITPLMYPASFFSVSTAYVLT 1652
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 -LALAVILQNMAAHWVLETHDGHQPOLTNRRLVLYAATFLPLNLV-VGAMXXXCSPSTA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; LENGTH: 1272
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7472

Query Match      5.4%; Score 92; DB 4; Length 1272;
Best Local Similarity 25.3%; Pred. No. 1.2;
Matches 80; Conservative 48; Mismatches 126; Indels 62; Gaps 17;

QY 3 ISALVLSCL---LTF-----LVLMRSLVT---HRLGSGSGD-----CQFSWNL--FSV 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 660 VDVLVSICVVFAMSFVPASFTLVLEERVTRAKHLQMLGSLPTLYWLNFLWDMCNLYV 719
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 PLPLPPLAGLVQOIIFFLGTALAFVLMPLVHGRNLL-----FFRSLESSWPFWLT 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 720 PACIVVLIIFLAFOORA-YVAPANLPALLLLLLLYGWSITPLMYPASFFSVSTAYVLT 778
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 -LALAVILQNMAAHWVLETHDGHQPOLTNRRLVLYAATFLPLNLV-VGAMXXXCSPSTA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 779 CINLFIGINGSMATFVLELFSQKLOEVSRL-ILKQVFLIFPHFCLGRGLIDMVRNQAWA 836
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 IRHPTPGYTYRNFLEKIEVSQSH-----PAMTAFCSLLQAQSL---PRTMAAPQD 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 DAFERLGDROFQSPLEWVGKLLAMVIQGPLFLF-TLLQHRSQLLPQPRVSLP-- 893
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 SLRPGDEEGMQLQTKDSMAKARGP-----AXRGRARWGLAYTLHNPLOVF 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 894 --LLGEDE--DVARERERVQATQGDVLRNLTKYRGQRMAMPADVRLCIGIPGECF 949
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 254 RKTALLGANGAQCPS 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 950 ---GLLVNGAGKTST 962
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-09-902-540-12884
; Sequence 12884, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12884
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12884

Query Match      5.3%; Score 90.5; DB 4; Length 557;
Best Local Similarity 30.9%; Pred. No. 0.58;
Matches 50; Conservative 11; Mismatches 52; Indels 49; Gaps 10;

QY 5 ALVLSCLLTFVLMRSLVTHRLGSGG-----SGDQFQSWNLFVPLPLPLAGLVQOII 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 242 AAQATSLLLAPMAMLVMTWALGRAGRVLRSAGKG-----LSRPFFPLGRAGLV----- 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 FLGTTAL--AFVLMPLVHGRNLLFFRSLESWP---FWLTALAVILQNMMAHW--VF 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 --LGAVSMTAAVLLVLLPL-----GAILLTSLQRSFGAALTWETLTL-----THWAGVL 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 LETHDGHQPOLTNRRLVLYAATFLPLNLVVGAMXXXCSPSIA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 338 LEPRTLH--ATGRSVLLAA-----GAGVLVCGGLGA 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; LENGTH: 1272
; TYPE: PRT
; ORGANISM: Human
US-08-714-741-34

Query Match      5.4%; Score 92; DB 4; Length 2146;
Best Local Similarity 25.3%; Pred. No. 2.5;
Matches 80; Conservative 48; Mismatches 126; Indels 62; Gaps 17;

QY 3 ISALVLSCL---LTF-----LVLMRSLVT---HRLGSGSGD-----CQFSWNL--FSV 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1534 VDVLVSICVVFAMSFVPASFTLVLEERVTRAKHLQMLGSLPTLYWLNFLWDMCNLYV 1593
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 PLPLPPLAGLVQOIIFFLGTALAFVLMPLVHGRNLL-----FFRSLESSWPFWLT 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1594 PACIVVLIIFLAFOORA-YVAPANLPALLLLLLLYGWSITPLMYPASFFSVSTAYVLT 1652
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 -LALAVILQNMAAHWVLETHDGHQPOLTNRRLVLYAATFLPLNLV-VGAMXXXCSPSTA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

; LENGTH: 1272
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7472

Query Match      5.4%; Score 92; DB 4; Length 1272;
Best Local Similarity 25.3%; Pred. No. 1.2;
Matches 80; Conservative 48; Mismatches 126; Indels 62; Gaps 17;

QY 3 ISALVLSCL---LTF-----LVLMRSLVT---HRLGSGSGD-----CQFSWNL--FSV 43
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 660 VDVLVSICVVFAMSFVPASFTLVLEERVTRAKHLQMLGSLPTLYWLNFLWDMCNLYV 719
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 44 PLPLPPLAGLVQOIIFFLGTALAFVLMPLVHGRNLL-----FFRSLESSWPFWLT 96
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 720 PACIVVLIIFLAFOORA-YVAPANLPALLLLLLLYGWSITPLMYPASFFSVSTAYVLT 778
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 97 -LALAVILQNMAAHWVLETHDGHQPOLTNRRLVLYAATFLPLNLV-VGAMXXXCSPSTA 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 779 CINLFIGINGSMATFVLELFSQKLOEVSRL-ILKQVFLIFPHFCLGRGLIDMVRNQAWA 836
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 155 IRHPTPGYTYRNFLEKIEVSQSH-----PAMTAFCSLLQAQSL---PRTMAAPQD 203
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 837 DAFERLGDROFQSPLEWVGKLLAMVIQGPLFLF-TLLQHRSQLLPQPRVSLP-- 893
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 204 SLRPGDEEGMQLQTKDSMAKARGP-----AXRGRARWGLAYTLHNPLOVF 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 894 --LLGEDE--DVARERERVQATQGDVLRNLTKYRGQRMAMPADVRLCIGIPGECF 949
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 254 RKTALLGANGAQCPS 269
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 950 ---GLLVNGAGKTST 962
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-08-714-741-34
; Sequence 34, Application US/08714741
; Patent No. 6500613
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
; APPLICANT: McDaniel, Larry S.
; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; AND USES OF SUCH GENES,
; EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; AND PRODUCTS
; TITLE OF INVENTION: EXPRESSION PRODUCTS
; NUMBER OF INVENTION: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
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Search completed: February 8, 2005, 13:42:12
Job time : 40.4542 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:32:20 ; Search time 108.54 Seconds
(without alignments)
975.246 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYSALVSLCLTLFLVLRMS.....APPTLWESQGFWRKLVG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	99.1	325	10	US-09-816-653A-4
2	1110.5	65.5	560	10	US-09-863-776-69
3	1110.5	65.5	599	15	US-10-104-047-2306
4	1110.5	65.5	667	9	US-09-759-056-2
5	1110.5	65.5	667	9	US-09-901-812-2
6	1110.5	65.5	667	10	US-09-863-776-32
7	1110.5	65.5	667	10	US-09-863-776-67
8	1110.5	65.5	667	14	US-10-227-884-80
9	1110.5	65.5	667	14	US-10-230-163-80
10	1110.5	65.5	667	14	US-10-230-338-80
11	1110.5	65.5	667	14	US-10-218-631-80
12	1110.5	65.5	667	14	US-10-230-414-80
13	1110.5	65.5	667	14	US-10-232-224-80

14	1110.5	65.5	667	14	US-10-216-159A-80	Sequence 80, Appl
15	1110.5	65.5	667	14	US-10-218-849-80	Sequence 80, Appl
16	1110.5	65.5	667	14	US-10-227-873-80	Sequence 80, Appl
17	1110.5	65.5	667	14	US-10-227-883-80	Sequence 80, Appl
18	1110.5	65.5	667	14	US-10-219-076-80	Sequence 80, Appl
19	1110.5	65.5	667	14	US-10-230-434-80	Sequence 80, Appl
20	1110.5	65.5	667	14	US-10-219-003-80	Sequence 80, Appl
21	1110.5	65.5	667	14	US-10-219-075-80	Sequence 80, Appl
22	1110.5	65.5	667	14	US-10-219-464-80	Sequence 80, Appl
23	1110.5	65.5	667	14	US-10-219-466-80	Sequence 80, Appl
24	1110.5	65.5	667	14	US-10-219-479-80	Sequence 80, Appl
25	1110.5	65.5	667	14	US-10-219-481-80	Sequence 80, Appl
26	1110.5	65.5	667	14	US-10-230-260-80	Sequence 80, Appl
27	1110.5	65.5	667	14	US-10-232-231-80	Sequence 80, Appl
28	1110.5	65.5	667	14	US-10-232-233-80	Sequence 80, Appl
29	1110.5	65.5	667	14	US-10-216-165-80	Sequence 80, Appl
30	1110.5	65.5	667	14	US-10-218-956-80	Sequence 80, Appl
31	1110.5	65.5	667	14	US-10-219-468-80	Sequence 80, Appl
32	1110.5	65.5	667	14	US-10-219-478-80	Sequence 80, Appl
33	1110.5	65.5	667	14	US-10-219-536-80	Sequence 80, Appl
34	1110.5	65.5	667	14	US-10-233-205-80	Sequence 80, Appl
35	1110.5	65.5	667	14	US-10-219-072-80	Sequence 80, Appl
36	1110.5	65.5	667	14	US-10-219-470-80	Sequence 80, Appl
37	1110.5	65.5	667	14	US-10-219-524-80	Sequence 80, Appl
38	1110.5	65.5	667	14	US-10-219-528-80	Sequence 80, Appl
39	1110.5	65.5	667	14	US-10-227-880-80	Sequence 80, Appl
40	1110.5	65.5	667	14	US-10-227-881-80	Sequence 80, Appl
41	1110.5	65.5	667	14	US-10-227-882-80	Sequence 80, Appl
42	1110.5	65.5	667	14	US-10-230-436-80	Sequence 80, Appl
43	1110.5	65.5	667	14	US-10-232-223-80	Sequence 80, Appl
44	1110.5	65.5	667	14	US-10-232-225-80	Sequence 80, Appl
45	1110.5	65.5	667	14	US-10-232-225-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-816-653A-4
Sequence 4, Application US/09816653A
Publication No. US20030021788A1
GENERAL INFORMATION:
APPLICANT: Rastelli, Luca
APPLICANT: Pennica, Diane
TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE SA
FILE REFERENCE: 10716/57
CURRENT APPLICATION NUMBER: US/09/816,653A
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/191,532
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens hSTRA6 polypeptide fragment, carboxy terminus
FEATURES:
NAME/KEY: MISC FEATURE
LOCATION: (146)..(148)
OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
NAME/KEY: MISC FEATURE
LOCATION: (232)..(232)
OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
NAME/KEY: MISC FEATURE
LOCATION: (290)..(290)
OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
NAME/KEY: MISC FEATURE
LOCATION: (292)..(292)
OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
NAME/KEY: MISC FEATURE
LOCATION: (302)..(302)
OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
NAME/KEY: MISC FEATURE

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; LOCATION: (303)...(303)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unknown
US-09-816-653A-4

Query Match
Best Local Similarity 99.1%; Score 1679; DB 10; Length 325;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSALVLSCLTFLVLMRSLVTHRLGSGGSDGQFSNWLSPVLPPLAGLLVQOIIIF 60
DB 1 CYSALVLSCLTFLVLMRSLVTHRLGSGGSDGQFSNWLSPVLPPLAGLLVQOIIIF 60
QY 61 FLGTTALAFVLMVPHVHGNLLFFRSLESSPFWLTLALAVLQNNAAHWVFLFTHDGH 120
DB 61 FLGTTALAFVLMVPHVHGNLLFFRSLESSPFWLTLALAVLQNNAAHWVFLFTHDGH 120
QY 121 QLTNRRLVYAATFLFPLNLVGMXXXCSPSIAIRHPTPGYTYRNFLKIEVSQSH 180
DB 121 QLTNRRLVYAATFLFPLNLVGMXXXCSPSIAIRHPTPGYTYRNFLKIEVSQSH 180
QY 181 TAFCSILLQAOQLLPRTHAOPDSLRPGDEDEGMQLLOTKDSMAKGARPGAXRGARW 240
DB 181 TAFCSILLQAOQLLPRTHAOPDSLRPGDEDEGMQLLOTKDSMAKGARPGAXRGARW 240
QY 241 AVTLAHNPTLOVFRKTALLGANGAOPCSSLPSPSITPAMOPAGPPDHXGXVEVCLH 300
DB 241 AVTLAHNPTLOVFRKTALLGANGAOPCSSLPSPSITPAMOPAGPPDHXGXVEVCLH 300
QY 301 PXXGSAPPTWLWESQGGFWRKXLVG 325
DB 301 PXXGSAPPTWLWESQGGFWRKXLVG 325

RESULT 2
US-09-863-776-69
; Sequence 69, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Mishra, Viahnu
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderu, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Li, Li
; APPLICANT: Taupier, Raymond J
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-020
; CURRENT APPLICATION NUMBER: US/09/863,776
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/206,679
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,688
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/206,829
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/207,748
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/207,798
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/208,263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 60/208,831
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/209,451
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/210,060
; PRIOR FILING DATE: 2000-06-07
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; PRIOR APPLICATION NUMBER: 60/219,507
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/221,317
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/221,927
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/263,135
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,688
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/263,694
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-863-776-69

Query Match 65.5%; Score 1110.5; DB 10; Length 560;
Best Local Similarity 76.6%; Pred. No. 3.4e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CYSALVLSCLTFLVLMRSLVTHRLGSGGSDGQFSNWLSPVLPPLAGLLVQOIIIF 42
DB 258 CYSALVLSCLTFLVLMRSLVTHRLGSGGSDGQFSNWLSPVLPPLAGLLVQOIIIF 42
QY 43 VPLPLPPLAGLLVQOIIIFLGTTLAFVLMVPHVHGNLLFFRSLESSPFWLTLALAVI 102
DB 318 AYQTAFTCLGLLVQOIIIFLGTTLAFVLMVPHVHGNLLFFRSLESSPFWLTLALAVI 377
QY 103 LQNNAAHWVFLFTHDGHQPLTNRRLVYAATFLFPLNLVGMXXXC 149
DB 378 LQNNAAHWVFLFTHDGHQPLTNRRLVYAATFLFPLNLVGMXXXC 437
QY 150 -SPSIAIRHP-----TFGYTYRNFLKIEVSQSHPAMTAFCSILLQAOQLLPRTHAOP 203
DB 438 QMDLSLLPPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSILLQAOQLLPRTHAOP 497
QY 204 SLRPGDEDEGMQLLOTKDSMAKGARPGAXRGARWGLAYTLAHNPTLOVFRKTALLGANG 263
DB 498 SLRPGDEDEGMQLLOTKDSMAKGARPGAXRGARWGLAYTLAHNPTLOVFRKTALLGANG 557
QY 264 AQP 266
DB 558 AQP 560

RESULT 3
US-10-104-047-2306
; Sequence 2306, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2306
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2306

Query Match 65.5%; Score 1110.5; DB 15; Length 599;
Best Local Similarity 76.6%; Pred. No. 3.7e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
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QY 1 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB 297 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 356
QY 43 VPLPLPPLAGLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 357 AYQTAFICGLLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 416
QY 103 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 149
DB 417 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 476
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 477 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 536
QY 204 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 263
DB 537 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 596
QY 264 AQP 266
DB 597 AQP 599

RESULT 4

US-09-759-056-2
; Sequence 2, Application US/09759056
; Patent No. US20020156252A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William L.
; TITLE OF INVENTION: NO. US20020156252A1el STRA6 Polypeptides
; FILE REFERENCE: GENENT.2827A2
; CURRENT APPLICATION NUMBER: US/09/759,056
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/197089
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/175849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/228914
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-759-056-2

Query Match 65.5%; Score 1110.5; DB 9; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB 365 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 424
QY 43 VPLPLPPLAGLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 425 AYQTAFICGLLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 484
QY 103 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 149
DB 485 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604
QY 204 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 263

DB 605 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 664
QY 264 AQP 266
DB 665 AQP 667

RESULT 5

US-09-901-812-2
; Sequence 2, Application US/09901812
; Patent No. US20020173461A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Polakis, Paul
; APPLICANT: Szeto, Wayne
; TITLE OF INVENTION: UPREGULATION OF TUMOR ANTIGENS TO
; TITLE OF INVENTION: ENHANCE EFFICACY OF IMMUNOTHERAPY
; FILE REFERENCE: GENENT.083A
; CURRENT APPLICATION NUMBER: US/09/901,812
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/228,914
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/759,056
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/175,849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/197,089
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-812-2

Query Match 65.5%; Score 1110.5; DB 9; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 42
DB 365 CYSALVLSCLLTFVLVMSLVTHR-----LGSGGSGD-----GQFSWNLF 424
QY 43 VPLPLPPLAGLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 425 AYQTAFICGLLVVQIIFFLGTTALAFVLMPLVHGRNLLFFRSLESSWPFMTLALAVI 484
QY 103 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 149
DB 485 LQNMAAHWVPLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604
QY 204 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 263
DB 605 SLRPGDEGMQLLQTKDSMAKGARPGASGRARWGLAYTLHNPQLQVFRKTALLGANG 664
QY 264 AQP 266
DB 665 AQP 667

RESULT 6

US-09-863-776-32
; Sequence 32, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T

Db 365 CYSALVLSCLLTFVLMSLVTHRTNLRALHGAALDLSPLHRSPHPSRQAFQWMSFS 424
Qy 43 VPLPLPPLAGLVVQIIFLGTALAFVLVMPVLHGRNLLFRSLSSWPFMLTLALAVI 102
Db 425 AVQTAFICLGLLVQIIFLGTALAFVLVMPVLHGRNLLFRSLSSWPFMLTLALAVI 484
Qy 103 LQNMAAHWVLETHDGHQPQTNRRVLYAATFLLPFLNLVGVAMXXXC----- 149
Db 485 LQNMAAHWVLETHDGHQPQTNRRVLYAATFLLPFLNLVGVAMVATRWVLSALYNAIHL 544
Qy 150 -SPSIAIRHP-----TFGYTYTNFKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
Db 545 GQMDLSLLPRAATLDPGYTYTNFKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604
Qy 204 SLRPGDEGMQLQTKDSNAKARGARVGLAYTLNPTLQVFRKTAGANG 263
Db 605 SLRPGDEGMQLQTKDSNAKARGARVGLAYTLNPTLQVFRKTAGANG 664
Qy 264 AQP 266
Db 665 AQP 667

RESULT 8
US-10-227-884-80
; Sequence 80, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Deenoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084411
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
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; PRIOR FILING DATE: 1998-06-18
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
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; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
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; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
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; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101922
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/106178

;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
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;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/130232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149638
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09

;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
;; PRIOR APPLICATION NUMBER: 60/169445
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.8%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

Qy 1 CYISALVLSCLLFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLFS 42
Db 365 CYISALVLSCLLFLVLMRSLVTHR-----GQFSWNLFS 424
Qy 43 VPLPLPLAGLVQOIIFFLGTGTALAFVLMVPMVHGRNLLFFRSLSSESWFFWTLALAVI 102
Db 425 AYQTAFICLGLVQOIIFFLGTGTALAFVLMVPMVHGRNLLFFRSLSSESWFFWTLALAVI 484
Qy 103 LQNMAAHWVLETHDGHQPLTNRRVLYAATFLPLNVLVGMXXXC----- 149
Db 485 LQNMAAHWVLETHDGHQPLTNRRVLYAATFLPLNVLVGMVATWRVLLSALYNAHL 544
Qy 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTMAAPQD 203
Db 545 GQMDLSLLPPRAATLDGYYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLLPRTMAAPQD 604
Qy 204 SLRPGDEEGMQLLOTXDSMAKGPAGXGRARWGLAYTLLENPTLOVERKLTALLGANG 263
Db 605 SLRPGDEEGMQLLOTXDSMAKGPAGXGRARWGLAYTLLENPTLOVERKLTALLGANG 664
Qy 264 AQP 266
Db 665 AQP 667

RESULT 9

US-10-230-163-80
; Sequence 80, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230.163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

PRIOR APPLICATION NUMBER: 60/101477	PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101786	PRIOR FILING DATE: 1998-09-25
PRIOR APPLICATION NUMBER: 60/101916	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101922	PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/106178	PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/106248	PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: 60/106464	PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106905	PRIOR FILING DATE: 1998-11-03
PRIOR APPLICATION NUMBER: 60/108787	PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108801	PRIOR FILING DATE: 1998-11-17
PRIOR APPLICATION NUMBER: 60/108849	PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112422	PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296	PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113605	PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621	PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115558	PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115565	PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115733	PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/119549	PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: 60/123618	PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/125259	PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: 60/125775	PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/126773	PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: 60/127887	PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/130232	PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/131022	PRIOR FILING DATE: 1999-04-26
PRIOR APPLICATION NUMBER: 60/131270	PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131291	PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131445	PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/134287	PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/140650	PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/140723	PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/141037	PRIOR FILING DATE: 1999-06-23
PRIOR APPLICATION NUMBER: 60/144758	PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/145698	PRIOR FILING DATE: 1999-07-20

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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
```

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Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
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QY 1 CYISALVLSCLTFLVLMRSVLYTHR-----LGSGGSGD-----GQFSWNLF 42
Db 365 CYISALVLSCLTFLVLMRSVLYTHR-----LGSGGSGD-----GQFSWNLF 424
QY 43 VPLPLPPLAGLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
Db 425 AYQTAFICLGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 484
QY 103 LQNMAAHWVFLTHDGHQPQLTNRRLVLYAATFLLPLNLVVGAMVATRWVLLSALYNAIHL 149
Db 485 LQNMAAHWVFLTHDGHQPQLTNRRLVLYAATFLLPLNLVVGAMVATRWVLLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAOSLLPRTMAAPQD 203
Db 545 QGMDLSLLPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAOSLLPRTMAAPQD 604
QY 204 SLRPGEEDEGMQLLOTQKDSMAKGARPGARWGLAYTLHNPFTLOVFRKTALLGANG 263
Db 605 SLRPGEEDEGMQLLOTQKDSMAKGARPGARWGLAYTLHNPFTLOVFRKTALLGANG 664
QY 264 AQP 266
Db 665 AQP 667
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RESULT 10
US-10-230-338-80
; Sequence 80, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC92
; CURRENT APPLICATION NUMBER: US/10/230,338
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
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; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-80
```

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Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
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QY 1 CYISALVLSCLTFLVLMRSVLYTHR-----LGSGGSGD-----GQFSWNLF 42
Db 365 CYISALVLSCLTFLVLMRSVLYTHR-----LGSGGSGD-----GQFSWNLF 424
QY 43 VPLPLPPLAGLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
Db 425 AYQTAFICLGLLVQOIIFFLGTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 484
QY 103 LQNMAAHWVFLTHDGHQPQLTNRRLVLYAATFLLPLNLVVGAMVATRWVLLSALYNAIHL 149
Db 485 LQNMAAHWVFLTHDGHQPQLTNRRLVLYAATFLLPLNLVVGAMVATRWVLLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAOSLLPRTMAAPQD 203
Db 545 QGMDLSLLPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLQAOSLLPRTMAAPQD 604
QY 204 SLRPGEEDEGMQLLOTQKDSMAKGARPGARWGLAYTLHNPFTLOVFRKTALLGANG 263
Db 605 SLRPGEEDEGMQLLOTQKDSMAKGARPGARWGLAYTLHNPFTLOVFRKTALLGANG 664
QY 264 AQP 266
Db 665 AQP 667
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RESULT 11
US-10-218-631-80
; Sequence 80, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
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FILE REFERENCE: P3530P1C14
CURRENT APPLICATION NUMBER: US/10/218,631
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 80
LENGTH: 667
TYPE: PRT
ORGANISM: Homo Sapien
US-10-218-631-80

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLFLVLMRSLVTHR-----LGGSGSD-----GQFSWNLF 42
DB 365 CYISALVLSCLLFLVLMRSLVTHRTNLRALHGAALDLSPLHRSPPHPSRQAIFCWNFS 424
QY 43 VPLPLPPLAGLVQVQIIFFLGTALAFVLMVPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 425 AYQATFICLGLLVQVQIIFFLGTALAFVLMVPLVHGRNLLFFRSLESSWPFMTLALAVI 484
QY 103 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLFPLNLVGMVATWRVLLSALYNAHL 149
DB 485 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLFPLNLVGMVATWRVLLSALYNAHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLPPRAATLDGYYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604
QY 204 SLRPGDEGMQLLOTQKDSMAKGARPGARWGLAYTLNHNPTLOVFRKTLALGANG 263
DB 605 SLRPGDEGMQLLOTQKDSMAKGARPGARWGLAYTLNHNPTLOVFRKTLALGANG 664
QY 264 AQP 266
DB 665 AQP 667

RESULT 12

US-10-230-414-80
Sequence 80, Application US/10230414
Publication No. US20030050448A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530P1C98
CURRENT APPLICATION NUMBER: US/10/230,414
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 80
LENGTH: 667
TYPE: PRT
ORGANISM: Homo Sapien
US-10-230-414-80

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYISALVLSCLLFLVLMRSLVTHR-----LGGSGSD-----GQFSWNLF 42
DB 365 CYISALVLSCLLFLVLMRSLVTHRTNLRALHGAALDLSPLHRSPPHPSRQAIFCWNFS 424
QY 43 VPLPLPPLAGLVQVQIIFFLGTALAFVLMVPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 425 AYQATFICLGLLVQVQIIFFLGTALAFVLMVPLVHGRNLLFFRSLESSWPFMTLALAVI 484
QY 103 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLFPLNLVGMVATWRVLLSALYNAHL 149
DB 485 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLFPLNLVGMVATWRVLLSALYNAHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 203
DB 545 GQMDLSLPPRAATLDGYYTYRNFLKIEVSQSHPAMTAFCSLLQAQSLPRTMAAPQD 604
QY 204 SLRPGDEGMQLLOTQKDSMAKGARPGARWGLAYTLNHNPTLOVFRKTLALGANG 263
DB 605 SLRPGDEGMQLLOTQKDSMAKGARPGARWGLAYTLNHNPTLOVFRKTLALGANG 664
QY 264 AQP 266
DB 665 AQP 667

RESULT 13

US-10-232-224-80
Sequence 80, Application US/10232224
Publication No. US20030065147A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC111
CURRENT APPLICATION NUMBER: US/10/232,224
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 80
LENGTH: 667
TYPE: PRT
ORGANISM: Homo Sapien
US-10-232-224-80

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLLTFLVLMRSVLTNR-----LGSGGSGD-----GQFSWNLF 42
DB 365 CYSALVLSCLLTFLVLMRSVLTNRALHARGAALDLSPLHRSRQAIFCWMSFS 424
QY 43 VPLPLPPLAGLLVQOIIFPLGTTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
DB 425 AYQTAFCIGLLVQOIIFPLGTTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 484
QY 103 LQMAAHWVLETHDGHQPOLNRRVLYAATFLLPLNVLVGAMXXXC----- 149
DB 485 LQMAAHWVLETHDGHQPOLNRRVLYAATFLLPLNVLVGAMVATRWLLSALYNATHL 544
QY 150 -SPSTAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLLAQSLPRTWAAPOD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLAQSLPRTWAAPOD 604
QY 204 SLRPGEEDEGMQLLOTQKDSMAKARGPGAXRGARWGLAYTLHNPPTLOVFRKTALLGANG 263
DB 605 SLRPGEEDEGMQLLOTQKDSMAKARGPGAXRGARWGLAYTLHNPPTLOVFRKTALLGANG 664
QY 264 AQP 266
DB 665 AQP 667

RESULT 14
US-10-216-159A-80
; Sequence 80, Application US/10216159A

Publication No. US20030069397A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Desnoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC6
CURRENT APPLICATION NUMBER: US/10/216,159A
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/064103
PRIOR FILING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 246
SEQ ID NO 80
LENGTH: 667
TYPE: PRT
ORGANISM: Homo Sapien
US-10-216-159A-80

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLLTFLVLMRSVLTNR-----LGSGGSGD-----GQFSWNLF 42
DB 365 CYSALVLSCLLTFLVLMRSVLTNRALHARGAALDLSPLHRSRQAIFCWMSFS 424
QY 43 VPLPLPPLAGLLVQOIIFPLGTTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 102
DB 425 AYQTAFCIGLLVQOIIFPLGTTALAFVLMVPLHGRNLLFRSLESSWPFWLTALAVI 484
QY 103 LQMAAHWVLETHDGHQPOLNRRVLYAATFLLPLNVLVGAMXXXC----- 149
DB 485 LQMAAHWVLETHDGHQPOLNRRVLYAATFLLPLNVLVGAMVATRWLLSALYNATHL 544
QY 150 -SPSTAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLLAQSLPRTWAAPOD 203
DB 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLAQSLPRTWAAPOD 604
QY 204 SLRPGEEDEGMQLLOTQKDSMAKARGPGAXRGARWGLAYTLHNPPTLOVFRKTALLGANG 263
DB 605 SLRPGEEDEGMQLLOTQKDSMAKARGPGAXRGARWGLAYTLHNPPTLOVFRKTALLGANG 664
QY 264 AQP 266
DB 665 AQP 667

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RESULT 15
US-10-218-849-80
; Sequence 80, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-80

Query Match      65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY      1  CYISALVLSCLLFLVLMRSLVTHR-----LGSGGSGD-----GQFSWNLF 42
Db      365  CYISALVLSCLLFLVLMRSLVTHRTNLRALHRCALDLSPLHRSHPSPQAFQWMSFS 424

QY      43  VPLPLPLAGLLVQQLIFFLGTALAFVLMVPMVHGRNLLFFRSLESSWPFMTLALAVI 102
Db      425  AYQTAFICLGLLVQQLIFFLGTALAFVLMVPMVHGRNLLFFRSLESSWPFMTLALAVI 484

QY      103  LQNMAAHWVLETHDGHQPQLTNRVLYAATFLFPLNLVGMXXC----- 149
Db      485  LQNMAAHWVLETHDGHQPQLTNRVLYAATFLFPLNLVGMVATWRVLLSALYNAIHL 544

QY      150  -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLQASLLPRTMAAPQD 203
Db      545  GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLQASLLPRTMAAPQD 604

QY      204  SLRPGEEDEGQQLLQTKDSMAKARPAGXGRARWGLAYTLHNPTLQVPRKTLALGANG 263
Db      605  SLRPGEEDEGQQLLQTKDSMAKARPAGXGRARWGLAYTLHNPTLQVPRKTLALGANG 664

QY      264  AQP 266
Db      665  AQP 667
```

Search completed: February 8, 2005, 13:45:13
Job time : 109.54 secs

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C:Accession: A38195
R:Cellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A:Title: Primary structure and functional expression of the human cardiac tetrodotoxin-
A:Reference number: A38195; MUID:92115699; PMID:130946
A:Accession: A38195
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-2016 <GEL>
A:Cross-references: UNIPROT:Q14524; GB:M77235; NID:gl84038; PIDN:AAA58644.1; PID:gl84039
A:Experimental source: heart
C:Superfamily: sodium channel protein
C:Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chan

Query Match 5.5%; Score 93; DB 2; Length 2016;
Best Local Similarity 23.8%; Pred. No. 14;
Matches 67; Conservative 31; Mismatches 113; Indels 70; Gaps 13;

QY 35 QFSNLFVPLPLPLAGLVQOITFFLQTTALFLVLMPLVHGRNLLFFRSLESSWPFW 94
DB 778 QCGWNIFD-----SIIVLSLMELGLSRMSNL---SVLSFELLRVFKLAKSWPTL 825
QY 95 -----LTLALAVILQNMMAHW-----FLETHGHQPLNMR-----RVLY 129
DB 826 NTLIKIIGNSVGALGNLTALVIFAVVGMQLFGKNYSRLRSDSGLLPRMHMDDFF 885
QY 130 AATFLLPLNLVVGAMXXCSPIAIRHPTPGYYTYRFLKIEVSQSHPMATFACSLLIQ 189
DB 886 HAFILIF--RIILCGEWIETWDCMEVSGQS---LCLLVLLVMVIGNLVLMFLIALLLS 940
QY 190 AOSLLPRTMAAPQDSLRPGEDEGMQLQTKDSMAKGPAGXAGRWGLAYTLL--HNP 248
DB 941 SFS-----ADNLTAPEDEBNNNLQ--ALARIQGLRFVXKRTTWDFFCGLLRHRP 989

QY 249 TLQVPRKTTALLGANGAQP--CSSLPGPSPTITPAMQAPGPD 288
DB 990 -----QKPAALAAQGLPSCIATPYSP-----PPE 1015

RESULT 3
T44942
cytochrome-c oxidase (EC 1.9.3.1) chain I [similarity] - Natronobacterium pharaonis
N:Alternate names: ba3-type cytochrome-c oxidase chain I
C:Species: Natronobacterium pharaonis
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44942
R:Mattar, S.; Engelhard, M.
Eur. J. Biochem. 250, 332-341, 1997
A:Title: Cytochrome ba3 from Natronobacterium pharaonis: An archaeal four-subunit cytoch
A:Reference number: 222876; MUID:98088958; PMID:9428682
A:Accession: T44942
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-581 <MAT>
A:Cross-references: UNIPROT:O07289; EMBL:Y10500; PIDN:CAA71525.1
A:Experimental source: strain SP1/28
C:Genetics:
A:Gene: cbaA
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated comple
F:228-232/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F:379/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 5.4%; Score 91.5; DB 2; Length 581;
Best Local Similarity 26.8%; Pred. No. 4.5;
Matches 63; Conservative 32; Mismatches 89; Indels 53; Gaps 15;

QY 6 LVLSCLLTTLVLMRSLVTHRLGSGSGDGFQSNLFSVPLPLPLAGLLVQOIIIFLGT 65
DB 300 LLLPSLLTAFTVVASMEHGARGQGS--GYFGW-LRALPWRDPVFTGMALGLMF----A 352
QY 66 ALAFLVMPVLHGRNLLFRSLESSW-----PFWLTALAVILQNMMAHWVLETHGHQPL 121

DB 353 AAAPSGM--VNAGMNIYLL--VHNTWVVGPHLTVGTAVALTPTMAVSYWFL-----PQ 402
QY 122 LTNER-----VLYAATFLLF-PLNLVVGAMXXCSPIAIRHPTPGYYTYRNFLEKIEVSQ 175
DB 403 ITGKKUMGKSVALLAQVVLVFGWTFMSNAMHRSGLAGMPRTAEP---QYRNF-EFEMAA 458
QY 176 SH----PAMTAFCSLLLAQASLL-----PRTMAAPQ--DSLRRPGEED 211
DB 459 GSGELNAQVVLGGILLFVSTLLFVLVVMVTLGDKAEPTLPANEVADTL-SGPED 514

RESULT 4
S18420
regulatory protein nifa - Azospirillum brasilense
C:Species: Azospirillum brasilense
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S18420
R:Liang, Y.Y.; Kaminski, P.A.; Elmerich, C.
Mol. Microbiol. 5, 2735-2744, 1991
A:Title: Identification of a nifa-like regulatory gene of Azospirillum brasilense Sp7 ex
A:Reference number: S18420; MUID:92140038; PMID:1779763
A:Accession: S18420
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-625 <Lia>
A:Cross-references: UNIPROT:P30667; EMBL:X60714; NID:G38677; PIDN:CAA43126.1; PID:G38678
C:Genetics:
A:Gene: nifa
C:Superfamily: Response regulator (sigma54-dependent transcriptional activator), PhlA ty
C:Keywords: DNA binding; P-loop; transcription regulation
F:205-426/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
F:233-240/Region: nucleotide-binding motif A (P-loop) #status atypical
F:300-304/Region: nucleotide-binding motif B

Query Match 5.3%; Score 90.5; DB 2; Length 625;
Best Local Similarity 27.7%; Pred. No. 5.9;
Matches 48; Conservative 9; Mismatches 55; Indels 61; Gaps 9;

QY 184 CSLLLQAQSL--PRTMAAPQDSLRPGEDEGMQLQTKDSMAKGA-----RFG---- 230
DB 447 CSLNLCNSSFVQRTTIGASVGGAP-----SMGPGAINRVPPRGPGPAA 492
QY 231 -----AXGRARWGLAYTLLHNPITLQVFRKTTALLGANG-----AQP 266
DB 493 ANAPKTPAMPAPVPEPAGAAAARGP---ARRVVRPLAGLRPPA--GGSGPPDPACP 546
QY 267 CSSLPGPSPTITPAMQAPGPDHGXVCLHWEPXKSGAPPTWLWESQQGF 319
DB 547 CPSRAPLPQAPPSPAPAAAPP---AAEVPLD-EPESGLRDLRLMAMERTGW 595

RESULT 5
C91079
probable cytochrome oxidase subunit [imported] - Escherichia coli (strain O157:H7, subst
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C91079
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91079
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <HAY>
A:Cross-references: UNIPROT:Q8X7Y2; GB:BA000007; PIDN:BA037026.1; PID:gl3363074; GSPDB:
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: Ecs3603
C:Superfamily: uncharacterized conserved protein YPO3363

Query Match 5.3%; Score 89.5; DB 2; Length 107;

Best Local Similarity 24.6%; Pred. No. 0.96;
Matches 28; Conservative 21; Mismatches 34; Indels 31; Gaps 5;

QY 33 DQGFNVLSPVLPPLPPLAGLLVQOIFFLGTALAFVLMVPL-HGRNLLFFRSLESSW 91
DB 18 DEETWS-----LPGAVV-----GFSWLFALAMPMLIYGSNTLFF--FIYTW 58

QY 92 PFWLTALAVILQNMAAHWVFLTHDGHQPOLTNRRLVYAATFLLPPLNVLVGM 145
DB 59 PFFLALMPVAVVGVIALH-----SLMDGKLRYISIVFTLMTVGMFGAL 101

RESULT 6
D85924
probable cytochrome oxidase subunit ygbE [imported] - Escherichia coli (strain O157:H7,
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85924
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: D85924
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <STO>
A:Cross-references: UNIPROT:Q8X72; GB:AE005174; NID:g12517203; PIDN:AG57856.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ygbE
C:Superfamily: uncharacterized conserved protein YPO3363

Query Match 5.3%; Score 89.5; DB 2; Length 107;
Best Local Similarity 24.6%; Pred. No. 0.96;
Matches 28; Conservative 21; Mismatches 34; Indels 31; Gaps 5;

QY 33 DQGFNVLSPVLPPLPPLAGLLVQOIFFLGTALAFVLMVPL-HGRNLLFFRSLESSW 91
DB 18 DEETWS-----LPGAVV-----GFSWLFALAMPMLIYGSNTLFF--FIYTW 58

QY 92 PFWLTALAVILQNMAAHWVFLTHDGHQPOLTNRRLVYAATFLLPPLNVLVGM 145
DB 59 PFFLALMPVAVVGVIALH-----SLMDGKLRYISIVFTLMTVGMFGAL 101

RESULT 7
S34364
hypothetical protein X - Salmonella typhimurium (fragment)
C:Species: Salmonella typhimurium
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: S34364
R:Persson, B.C.; Bjork, G.R.
submitted to the EMBL Data Library, June 1993
A:Description: Isolation of a gene (miaE) involved in hydroxylation of ms2106A in trna c
A:Reference number: S34359
A:Accession: S34364
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-268 <PER>
A:Cross-references: EMBL:X73368; NID:g312705; PIDN:CAA51785.1; PID:g312711

Query Match 5.3%; Score 89.5; DB 2; Length 268;
Best Local Similarity 26.2%; Pred. No. 2.7;
Matches 37; Conservative 20; Mismatches 45; Indels 39; Gaps 6;

QY 5 ALVLSCLTFLVLMRSIVTHRLSGSGDGGQGFNVLSPVLPPLPPLAGLLVQOIFFLGT 64
DB 27 ALFISVLVFIYIVSVLSLIEHGPGLG-----FTLP-----GLLI-AIIPFAV 70

QY 65 TALAFVLMVPLHGRNLLFFRSLESSWPFWLTALAVILQNMAAHWVFLTHDGHQPOLT 124
DB 71 KGLQYQAMTSLNGVHFGQCSMRRAW--WTMFALPVL--MVA----- 110

QY 125 RRVLYAATFLLPPLNVLVGM 145
DB 111 ---LYIVLYIISLVIAVGG 128

RESULT 8
WMBEH6
UL36 protein - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: I30085
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Per
J. Gen. Virol. 69, 1531-1574, 1988
A:Title: The complete DNA sequence of the long unique region in the genome of herpes sin
A:Reference number: A30083; MUID:88274327; PMID:2839594
A:Accession: I30085
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-3164 <MCG>
A:Cross-references: UNIPROT:P10220; GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g5953
C:Genetics:
A:Gene: UL36
C:Superfamily: varicella-zoster virus gene 22 protein

Query Match 5.3%; Score 89; DB 1; Length 3164;
Best Local Similarity 36.9%; Pred. No. 51;
Matches 24; Conservative 4; Mismatches 17; Indels 20; Gaps 3;

QY 247 NPTLQVFRKTTALLGANGAQCSSLGSPSITPMQPGPDHGXGVCLHWEPKXGSA 306
DB 2824 DPTAPV-----LGRNPAEFTSSPAGSPPPPAVQPVAPP-----PTSG-P 2863

QY 307 PPTWL 311
DB 2864 PPTYL 2868

RESULT 9
A65056
hypothetical protein in surE-cysC intergenic region - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A65056
R:Blattner, F.R.; Mau, B.; Shao, Y.
A:Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65056
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <BLAT>
A:Cross-references: UNIPROT:P46141; GB:AE000358; GB:U00096; NID:g2367156; PIDN:AAC75791
A:Experimental source: strain K-12, substrain MGL655
C:Genetics:
A:Gene: ygbE
C:Superfamily: uncharacterized conserved protein YPO3363

Query Match 5.2%; Score 88.5; DB 2; Length 107;
Best Local Similarity 24.6%; Pred. No. 1.2;
Matches 28; Conservative 21; Mismatches 34; Indels 31; Gaps 5;

QY 33 DQGFNVLSPVLPPLPPLAGLLVQOIFFLGTALAFVLMVPL-HGRNLLFFRSLESSW 91
DB 18 DEETWS-----LPGAVV-----GFSWLFALAMPMLIYGSNTLFF--FIYTW 58

QY 92 PFWLTALAVILQNMAAHWVFLTHDGHQPOLTNRRLVYAATFLLPPLNVLVGM 145
DB 59 PFFLALMPVAVVGVIALH-----SLMDGKLRYISIVFTLMTVGMFGAL 101

RESULT 10

Query Match	5.1%	Score 87;	DB 2;	Length 621;
Best Local Similarity	21.7%;	Pred. No. 12;		
Matches 38;	Conservative 28;	Mismatches 59;	Indels 50;	Gaps 8
QY	172	EVSQSHPWANTACSL	-----LIQ-----	AQSLLPRTMAAPQDSLRPGEDEBG 213
DB	4	DINSVESLNSACNNQSDTDTAPLLEDQHA	SNQGAASSRCQPQASPRQXWQRQSPVHI 63	
QY	214	MOLLQTKDSMAGARPGRAXRGRARWGLAYTL	LHNPTLQVFRKTALLGANGAQCPSLPGS 273	
DB	64	LRLQEEDQQLETA	-----SLPAIPNPPE-----LTGA-----	APGS 96
QY	274	PPSITPAM---	QPAGPP-DHXGXVEVCLHWEPPXXGAP-PTWLWSSQQQGFWRKKL 323	
DB	97	PPSVAPSSLPSPPSOPPAKHGRCCKEKI	WGNTRGNRGKKKIWRWQPPPGQLSKL 151	

A;Accession: AF0359
A;Status: preliminary
A:Molecule type: DNA
A:Residues: 1-528 <KUR>
A:Cross-references: UNIPROT:Q8ZCM3; GB:AL590842; PIDN:CAC92204.1; PID:g15980916; GSPDB:
C;Genetics:
A:Gene: sfuB
C;Superfamily: sfuB protein

Query Match 5.1%; Score 86; DB 2; Length 528;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 78; Conservative 31; Mismatches 129; Indels 112; Gaps 15;

QY 6 LVLSCLLTFLVLMRSLVTHRLGSGGQGFQSWNLFSVPLPLPLAGLLVQOIIFPLGTT 65
 Db 244 LALCCLGILLVATSGYHRYARVSGTGR-----RQTVYSGMGS 283
 QY 66 ALAFLVMPVLHGRNLLFRSLESSWPF-----WLT-----LAL 99
 Db 284 LTLCLLPL-----ITLTLGVPFITLWRSLSGIGDIWLNPELLPALKQTLGLAL 336
 QY 100 --AVILONMAHWVFLETHDGHLPOLNRRVLVAATFLLPLNVLGAMXXXCSPSTAIRH 157
 Db 337 SGAVITITLCAIPMAWLSVR--YFGRUHR-----AMECYVTSSLPGIVVALALVITIRI 390
 QY 158 PTPGYTYRNFLEKIEVSGHPAMTAFCSLLLOAQSLLPRTMAPODSLPGEGDEGMQLL 217
 Db 391 ARPLY-----QTEFTVLLAYLLMTFPRALI-----SLRAGIAQAPVELE 429
 QY 218 QTKDMSKMG-----ARPGAXRGRARWGLAYTLLHNPLOVFRKTTALLGANGAQ 265
 Db 430 NVARSILGRPTQAMLSTTLRLAAPGAAAGAA---LVFLAISNE---LTATLLAPNGTR 482
 QY 266 PCSLPGSPSITPAMQPAGPPDHKXGVEVCLHWEPXGSGAPPTWLWESQ 315
 Db 483 TLAT--GFWALTSEIDYVAAP--YAFLMVAL-----SLPUTWLLYSQ 521
 RESULT 14
 A:87673
 conserved hypothetical protein CC3419 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87673
 R:Nierman, W.C.; Feidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Leub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87673
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-582 <STO>
 A:Cross-references: UNIPROT:Q9A2Y7; GB:AB005673; NID:gl3425133; PIDN:AAK25381.1; GSPDB:G
 C:Genetics:
 A:Gene: CC3419

Query Match 5.1%; Score 86; DB 2; Length 582;
 Best Local Similarity 24.3%; Pred. No. 13;
 Matches 74; Conservative 30; Mismatches 113; Indels 88; Gaps 14;
 QY 62 LGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLTALAVILONMAHWVFL---ETHDG 118
 Db 220 VGLTLGLWLLPLMWLVIGGGFLATPFTGLAPLWGTAKAATALLSAAALILLINAAVQDG 279
 QY 119 H--PQLTNRRLVAATAFLLPLNVLVG-----AMXXXCSP 151
 Db 280 EEPHLIPCLAAIAGLLIPVILAGVALWLRIDQGLTPERVVAGVWLWVAGFTAGY 339
 QY 152 SIAIRHTPTPGYTYRNFLEKIEVSOSHAPMTAFCSLLL-----QAQSLL 194
 Db 340 ALAAVKPGP-----WNK-PLERTNPIMAAACVLLLIALLFTPIANPARLSVASQVKRLE 391
 QY 195 PRTMAAPQ-----DSLPRGEDEGMQLLQTKDS--MAKGARPGAXRGRARWGLAYTL 244
 Db 392 SGEVAADKDFQFLRFDRAGYGR--EALDRUKTHPNAEIAKRAADA-----ASTE 440
 QY 245 LHNPTLOV---FRKTALLGANGAQPCS-----SLGSPSPSITPAMQ-PA--GPPDHXGX 292
 Db 441 KQYPAGEIRPDPFKAMAVYPAGKALPQSFVAQDWQSPSGNSCTAIAQCPCALVADVADGK 500
 QY 293 VEVCLE 297
 Db 501 DEVL 505

RESULT 15
 S40085
 hypothetical protein 4 - Lactococcus lactis
 C:Species: Lactococcus lactis
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S40085
 R:Eaton, T.J.; Shearman, C.; Gasson, M.
 submitted to the EMBL Data Library, December 1993
 A:Description: Cloning and sequence analysis of the DNAK gene region of Lactococcus lac
 A:Reference number: S40082
 A:Accession: S40085
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-614 <EAT>
 A:Cross-references: UNIPROT:P42377; EMBL:X76642; NID:G435489; PIDN:CAA54090.1; PID:G435

Query Match 5.1%; Score 86; DB 2; Length 614;
 Best Local Similarity 19.9%; Pred. No. 14;
 Matches 49; Conservative 35; Mismatches 74; Indels 88; Gaps 11;
 QY 5 ALVLSCLLTFLVLMRSLVTHRLGSGGSGDQGFQSWNLFSV-----PLPLPLAGLLVQOI 58
 Db 332 SLIFSCFSLVLMQLPI-----FPWKLFSIFTIVQDPAREFTLGLF---- 374
 QY 59 IFPLGTTALAFVLMPLVHGRNLLFRSLESSWPFMTLTALAVILONMAHWVFLETHDG 118
 Db 375 -----SALSLLVLPIL-----LDKISGKTSYVLTIGLLVIFSIL-----G 410
 QY 119 HPQLTNR-----RVLYAA-----TFLLPLNVLGAMXXXCSPSIAIRHPTPGY 163
 Db 411 FAEFRNRIOKGSQPLFASQAQSLNKTPTFNYMENPDSIAIGEYL-----PQVIGSHNQPYEK 466
 QY 164 TYRNFLEKIE--VSQSHPAMTAFCSLLLOAQSLLPRTMAAPQDSLPRGEDEGMQLLQTKD 221
 Db 467 TIQQFYKDKNVYGMNRQAMT-----YLSORGKLPGLA-----KSIQISD 506
 QY 222 SMAKGA 227
 Db 507 YSKKGS 512
 Search completed: February 8, 2005, 13:41:06
 Job time : 34.1317 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 8, 2005, 13:21:20 ; Search time 142.653 Seconds
(without alignment)
1166.650 Million cell updates/sec

Title: US-09-816-653A-4

Perfect score: 1695

Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQGFWRKKLIVG 325

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot Q3:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1110.5	65.5	560	2 Q7L9G1	Q7L9G1 homo sapien
2	1110.5	65.5	667	2 Q8TB21	Q8TB21 homo sapien
3	1110.5	65.5	667	2 Q9BX79	Q9BX79 homo sapien
4	1110.5	65.5	708	2 Q7Z3U9	Q7Z3U9 homo sapien
5	1106.5	65.3	658	2 Q9BX78	Q9BX78 homo sapien
6	1022.5	60.3	286	2 Q71RB9	Q71RB9 mus sapien
7	832.5	49.1	670	2 Q70491	Q70491 mus musculus
8	832.5	49.1	670	2 Q6DIA8	Q6DIA8 mus musculus
9	133	7.8	322	2 Q69ZH3	Q69ZH3 mus musculus
10	133	7.8	621	2 Q8C716	Q8C716 mus musculus
11	133	7.8	621	2 Q9DBN1	Q9DBN1 m mus muscus
12	115.5	6.8	618	2 Q8PBV8	Q8PBV8 xanthomonas
13	100.5	5.9	572	2 Q7NYU4	Q7NYU4 chromobacte
14	100	5.9	2170	2 Q7TNJ2	Q7TNJ2 rattus norv
15	98.5	5.8	1841	2 Q9E60	Q9E60 mus musculus
16	98	5.8	525	2 Q6D2F7	Q6D2F7 erwinia car
17	97.5	5.8	403	1 GC5B HUMAN	GC5B homo sapien
18	97.5	5.8	494	2 Q7M5H9	Q7M5H9 wolfinella s
19	97	5.7	336	2 Q7NRX1	Q7NRX1 chromobacte
20	97	5.7	595	2 Q6ZRS5	Q6ZRS5 homo sapien
21	96.5	5.7	593	2 Q83179	Q83179 treponema p
22	96.5	5.7	1514	2 Q82BH0	Q82BH0 streptomyce
23	96	5.7	913	2 Q6CKC6	Q6CKC6 kluyveromyces
24	95.5	5.6	275	2 Q88BF0	Q88BF0 pseudomonas
25	95.5	5.6	526	2 Q8NP08	Q8NP08 corynebacte
26	95	5.6	273	2 Q7WAG2	Q7WAG2 bordetella
27	95	5.6	273	2 Q7WJK9	Q7WJK9 bordetella
28	94.5	5.6	378	2 Q71ES1	Q71ES1 betta anaba
29	94.5	5.6	482	2 Q8M258	Q8M258 pfisteria
30	94.5	5.6	540	2 Q69YS5	Q69YS5 homo sapien
31	94	5.5	465	2 Q72WP1	Q72WP1 desulfovibr

32	94	5.5	476	1 TR16 HUMAN	Q15654 homo sapien
33	93.5	5.5	378	2 Q6VVU0	Q6VVU0 herichthys
34	93	5.5	279	2 Q8DM47	Q8DM47 synchococc
35	93	5.5	1962	2 Q75RX9	Q75RX9 homo sapien
36	93	5.5	2016	1 C1N5 HUMAN	Q14524 homo sapien
37	93	5.5	2016	2 Q75RY0	Q75RY0 homo sapien
38	92.5	5.5	378	2 Q71ES2	Q71ES2 betta hippo
39	92	5.4	796	2 Q9P3B4	Q9P3B4 neurospora
40	92	5.4	2008	2 Q96S58	Q96S58 homo sapien
41	92	5.4	2146	2 Q81ZV2	Q81ZV2 homo sapien
42	92	5.4	2146	2 Q9BZC4	Q9BZC4 homo sapien
43	92	5.4	2146	2 Q9NR73	Q9NR73 homo sapien
44	91.5	5.4	353	2 Q8M629	Q8M629 pfisteria
45	91.5	5.4	378	2 Q71ES3	Q71ES3 betta pi. c

ALIGNMENTS

RESULT 1

ID	Q7L9G1	PRELIMINARY;	PRT;	560 AA.
AC	Q7L9G1;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein FLJ12541.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	PubMed14702039; DOI=10.1038/ng1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,			
RA	Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,			
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,			
RA	Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,			
RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA	Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba Y., Ishida S.,			
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,			
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,			
RA	Togiyasu S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,			
RA	Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Momiya A., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikemura Y., Okamoto S.,			
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,			
RA	Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,			
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,			
RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,			
RT	"Complete sequencing and characterization of 21,243 full-length human			
RT	CDNAs."			
RL	Nat. Genet. 36:40-45(2004).			
RL	EMBL; AK022603; BAB14122.1; -.			
SQ	SEQUENCE 560 AA; 61987 MW; DF0FFED7687AED74 CRC64;			

Query Match 65.5%; Score 1110.5; DB 2; Length 560;
Best Local Similarity 76.6%; Pred. No. 2.3e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

QY 1 CVISALVLSCLLTFLVLMRSVLVTHR-----LGGSGSGD-----GQFSWNLF 42

Db	258	CYISALVLSCLTFLVLMSRLSVTRTNLRHRCALDLSPLHRSPPHRSQAIFCWMSPS	317
Qy	43	VLPPLPPLAGLIVQOIIIFLGTGTTALAFVLMPVLHGNTLFFSLSSPPFWLTLALAVI	102
Db	318	AYQTAFICIGLVQOIIIFLGTGTTALAFVLMPVLHGNTLFFSLSSPPFWLTLALAVI	377
Qy	103	LQNMAAHVVFLETHDGHQPOLNRRVLVAATFLPLNLVVGAMKXXC-----	149
Db	378	LQNMAAHVVFLETHDGHQPOLNRRVLVAATFLPLNLVVGAMVATRWVLSALYNAIHL	437
Qy	150	-SPSIAIRHP-----TPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPOD	203
Db	438	GQMDLSLLPPRAATLDPGYTYRNFLEKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPOD	497
Qy	204	SURPGEDEGMQLLTKDSMAKARGPAGXRGARAGWGLAYTLHNPITLOVFRKTLALGANG	263
Db	498	SURPGEDEGMQLLTKDSMAKARGPAGXRGARAGWGLAYTLHNPITLOVFRKTLALGANG	557
Qy	264	AQP 266	
Db	558	AQP 560	
RESULT 2			
ID	Q8TB21	PRELIMINARY; PRT; 667 AA.	
OT	Q8TB21;		
DT	01-JUN-2002	(TrEMBLrel. 21, Created)	
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)	
DE	01-OCT-2002	(TrEMBLrel. 22, Last annotation update)	
DE		Stimulated by retinoic acid gene 6.	
GN		Name=FLJ12541;	
OS		Homo sapiens (Human).	
OC		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX		NCBI_Taxid=9606;	
RN	[1]		
RN		SEQUENCE FROM N.A.	
RC		TISSUE=Brain;	
RC		MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA		Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA		Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA		Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA		Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,	
RA		Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA		Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA		Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA		Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,	
RA		Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA		Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA		Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA		Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	
RA		Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA		Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA		Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA		Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA		Jones S.J., Marra M.A.;	
RT		"Generation and initial analysis of more than 15,000 full-length human	
RT		and mouse cDNA sequences."	
RL		Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RL		[2]	
RN		SEQUENCE FROM N.A.	
RP		TISSUE=Brain;	
RC		TISSUE=Brain;	
RA		Strausberg R.;	
RL		Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
DR		EMBL: BC025256; AHA25256.1; -	
EQ		SEQUENCE 667 AA; 73532 MW; 120685F4635CE0E5 CRC64;	
Query Match		65.5%; Score 110.5; DB 2; Length 667;	
Best Local Similarity		76.6%; Pred. No. 2.8e-81;	
Matches 232; Conservative		4; Mismatches 30; Indels 37; Gaps	

Db 365 CYSALVLSCLTFLVLMRSLVTHRTNLRALHGAALDLSPLRSPHPSRQAIFCWMSEFS 424
QY 43 VPLPPLPPLAGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 102
Db 425 AYQTAFICGLGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 484
QY 103 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMXXXC----- 149
Db 485 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 544
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 203
Db 545 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 604
QY 204 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 263
Db 605 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 664
QY 264 AQP 266
Db 665 AQP 667

RESULT 4
Q723U9 PRELIMINARY; PRT; 708 AA.
AC Q723U9
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypochemical protein DKF2p6686p1959 (Fragment).
GN Name=DKF2p6686p1959;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human endometrium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Oanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX537413; CAD97655.1; -
KW Hypochemical protein.
FT NON TER 1
SQ SEQUENCE 708 AA; 77825 MW; DB88B84AEAD286ED CRC64;

Query Match 65.5%; Score 1110.5; DB 2; Length 708;
Best Local Similarity 76.6%; Pred. No. 3e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLTFLVLMRSLVTHR-----LGGSGSGD-----GQFSWNLF 42
Db 406 CYSALVLSCLTFLVLMRSLVTHRTNLRALHGAALDLSPLHPSRQAIFCWMSEFS 465
QY 43 VPLPPLPPLAGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 102
Db 466 AYQTAFICGLGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 525
QY 103 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMXXXC----- 149
Db 526 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 585
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 203
Db 586 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 645
QY 204 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 263
Db 646 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 705
QY 264 AQP 266

Db 706 AQP 708
PRELIMINARY; PRT; 658 AA.
Q9BX78
ID Q9BX78
AC Q9BX78
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE STRA6 isoform 2.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RA "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bruch J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF352729; AAK30290.1; -
DR EMBL; AY358748; AAK89108.1; -
SQ SEQUENCE 658 AA; 72582 MW; 5405281727F647DD CRC64;
Query Match 65.3%; Score 1106.5; DB 2; Length 658;
Best Local Similarity 76.2%; Pred. No. 5.7e-81;
Matches 231; Conservative 5; Mismatches 30; Indels 37; Gaps 4;
QY 1 CYSALVLSCLTFLVLMRSLVTHR-----LGGSGSGD-----GQFSWNLF 42
Db 356 CYSALVLSCLTFLVLMRSLVTHRTNLRALHGAALDLSPLRSPHPSRQAIFCWMSEFS 415
QY 43 VPLPPLPPLAGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 102
Db 416 AYQTAFICGLGLVQVQIIFFLGTTALAFVLMVPLHGRNLLFFRSLESSWPFMTLALAVI 475
QY 103 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMXXXC----- 149
Db 476 LQNMAAHWVLETHDGHQPQLTNRRLVYAATFLLPPLNVLVGAMVATRWVLLSALYNAIHL 535
QY 150 -SPSIAIRHP-----TPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 203
Db 536 GQMDLSLLPRAATLDPGYTYRNFLKIEVSQSHPAMTAFCSLLLOAQSLPRTMAAPQD 595
QY 204 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 263
Db 596 SLRPGDEEGMQLQTKDSMAKARGPCAGRGARWGLAYTLHNPFLQVFRKTALLGANG 655
QY 264 AQP 266

```

Db      656 AQP 658

RESULT 6
Q71RB9 PRELIMINARY; PRT; 286 AA.
AC Q71RB9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein PPI4296.
CN Name=PPI4296;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wan D.F., Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Zu J.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF370419; AAQ15255.1; -
KW Hypothetical protein.
SQ SEQUENCE 286 AA; 31877 MW; 24B6AG20844A5EFB CRC64;

Query Match 60.3%; Score 1022.5; DB 2; Length 286;
Best Local Similarity 74.8%; Pred. No. 1.4e-74;
Matches 214; Conservative 5; Mismatches 30; Indels 37; Gaps 4;

Qy 18 MRLSVTHR-----LGSGGSGD-----GQFSNLFSPVLPPLPPLAGLLVQII 59
Db 1 MRLSVTHRNLRALHGAALDLSPLRSPHPSRQAFQWMSFSAYQTAFICGLGLVQII 60
Qy 60 PFLGTTALAFVLMVPLHGRNLLFRSLESSWPFMTALAVILQNAHAAHVFLTHDGH 119
Db 61 PFLGTTALAFVLMVPLHGRNLLFRSLESSWPFMTALAVILQNAHAAHVFLTHDGH 120
Qy 120 POLTNRRLVYAATFLPLNLVGMXXC-----SPSIAIRHP-----TP 160
Db 121 POLTNRRLVYAATFLPLNLVGMXXC-----SPSIAIRHP-----TP 180
Qy 161 GYTYRNFLKIEVSQSHPAMTAFCSLLQAOQLPRTMAAPQDSLRPGEDEGMQLQTK 220
Db 181 GYTYRNFLKIEVSQSHPAMTAFCSLLQAOQLPRTMAAPQDSLRPGEDEGMQLQTK 240
Qy 221 DSMAGARPAGRGARWGLAYTLHNPTLOVRKTKALLGANGAQP 266
Db 241 DSMAGARPAGRGARWGLAYTLHNPTLOVRKTKALLGANGAQP 286

RESULT 7
O70491 PRELIMINARY; PRT; 670 AA.
ID O70491
AC O70491;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Retinoic acid-responsive protein.
CN Name=Strag6;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA Schubaur B., Dolle P., Chambon P.;
RT "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT embryonal carcinoma cells and characterization of a novel mouse gene,
RL Stral (mouse LERK-2/Bp1g2).";
RL Dev. Biol. 170:420-433 (1995).
RN [2]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97346723; PubMed=92031140; DOI=10.1016/S0925-4773(97)00039-7;
RA Bouillet P., Sapin V., Chazaud C., Messaddeq N., Decimo D., Dolle P.,
RA Chambon P.;
RT "Developmental expression pattern of Stra6, a retinoic acid-responsive
RT gene encoding a new type of membrane protein.";
RL Mech. Dev. 63:173-186 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Bouillet P.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF062476; AAC16016.1; -
DR MGD; MGI:107742; Stra6.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 670 AA; 73774 MW; 6ACB69F3EE16A4F7 CRC64;

Query Match 49.1%; Score 832.5; DB 2; Length 670;
Best Local Similarity 57.7%; Pred. No. 8.1e-59;
Matches 176; Conservative 28; Mismatches 62; Indels 39; Gaps 4;

Qy 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSNLF 42
Db 366 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-----GQFSNLF 425
Qy 43 VPLPPLAGLLVQIIIFLGTALAFVLMVPLHGRNLLFRSLESSWPFMTALAVI 102
Db 426 AYQTAFSCGLLVQVIFFLGTTSLAFVPLHGRNLLFRSLESSWPFMTALAVI 485
Qy 103 LQNAHAAHVFLTHDGHGHPOLTNRRLVYAATFLPLNLVGMXXCSPSIAIRHP--- 159
Db 486 LQNAHAAHVFLTHDGHGHPOLTNRRLVYAATFLPLNLVGMXXCSPSIAIRHP--- 545
Qy 160 -----PGYTYRNFLKIEVSQSHPAMTAFCSLLQAOQLPRTMAAPQD 203
Db 546 QOWDLSLLPORAASLDGTYHYQNFLEIASQSHPGVIAFCALLHAPSPPPLAPQD 605
Qy 204 SLRPEDEGMQLQTKDSMAKARPAGRGARWGLAYTLHNPTLOVRKTKALLG--A 261
Db 606 SLRPAEEEGMQLQTKDLMAKAGHGKGSOSRARGWGLAYTLHNPTLOVRKTKALLG--A 665
Qy 262 NGROP 266
Db 666 NGTOP 670

RESULT 8
Q6DIA8 PRELIMINARY; PRT; 670 AA.
ID Q6DIA8
AC Q6DIA8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Stra6 protein.
CN Name=Strag6;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smillius D.E., Schnerch J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC075657; AH75657.1; --
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 670 AA; 73715 MW; 96F963788EF91249 CRC64;

Query Match 49.1%; Score 832.5; DB 2; Length 670;
Best Local Similarity 57.7%; Pred. No. 8.1e-59;
Matches 176; Conservative 28; Mismatches 62; Indels 39; Gaps 4;

QY 1 CYISALVLSCLLTFVLVRLSLVTHR-----LGGSGSD-----GQFSNPLFS 42
DB 366 CYISALVLSCASTFLLIRSLRTHANLQALHRAALDLPPLQSIHPSRQAIVSWMFC 425
QY 43 VPLPLPPLAGLIVQOIIFFLGTGTTALAPLVLMVPLVHGRNLLFFRSLESSWPFMTLALAVI 102
DB 426 AYOTAFSCGLVQVQVIFLGTGTTSLAPLVFVPLVHGRNLLLSLESFTWFWLUTVALAVI 485
QY 103 LQNAAHVPLETHDGHQPQITNRRLVYAATFLFPLNVLVGMXXXCSPSIAIRHPT--- 159
DB 486 LQNIANWIFLTHGHGPELTNRMLCVATFLFPLNVLVGMXXXCSPSIAIRHPT--- 545
QY 160 -----PGYTYNRFNKIEVSQSHPMATFCSLLLOAQSLPRTMAPOD 203
DB 546 GQMDLSLLPQRAASLDPGYTYNRFNKIEVSQSHPMATFCSLLLOAQSLPRTMAPOD 605
QY 204 SIRGEDEGMQLLOTQKDSMAKARPAGXRGARWGLAYTLHNPFTLOVPRKTKALLG--A 261
DB 606 SLRPAEEEGQLLOTQKDLMAKAGHKGQSQRARWGLAYTLHNPFTLOVPRKTKALLG--A 665
QY 262 NGAQP 266
DB 666 NGTQP 670

RESULT 9
Q69ZH3 PRELIMINARY; PRT; 322 AA.
AC Q69ZH3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE MKTAA1529 protein (Fragment).
GN Name=MKTAA1529;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic intestinal tract;
RA Okazaki N., Kikuno N.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA Nagase T., Ohara O., Koga H.;
RT "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
Randomly Sampled from Size-Fractionated Libraries.";
RL DNA Res. 11:205-218(2004).
DR ENBL; AK173193; BAD32471.1; --
FT NON TER 1
SQ SEQUENCE 322 AA; 36477 MW; AD7B68DFC7A34578 CRC64;

Query Match 7.8%; Score 133; DB 2; Length 322;
Best Local Similarity 23.1%; Pred. No. 0.012;
Matches 55; Conservative 37; Mismatches 92; Indels 54; Gaps 7;
QY 50 LAGLIVQOIIFFLGTGTTALAPLVLMVPLVHGRNLLFFRSLESSWPFMTLALAV---ILQNM 106
DB 89 LMGYLIIHVQSLCGVLMYGLVLPITIIHRGL---EMLQGLGLVLTLSIVVGLIILQVM 145
QY 107 AAHWVPLETHDGHQPQ-----LTNRRLVYAATFLFPLNVLVGMXXXCSPSIAI----- 155
DB 146 IAGTFFLOPKLGTSDKQKPLANNRRAFHNFYFFYNVLG--LGACLSRLILSCLLG 203
QY 156 -----RHPTPGYTYNRFNKIEVSQSHPMATFCSLLLOAQSLPRTMA 199
DB 204 TWLIARIDRTIMQSGVEGADMGFGAWIGMLFVDHYHTNPVLSFCHILITS----- 254
QY 200 APODSLURPGEDEGMQLLOTQKDSMAKARPAGXRGARWGLAYTLHNPFTLOVPRKT 256
DB 255 -----HKDKLQKTVKVMCLNQSGAGPRFSARTRFWLQTLLNNPRLVMLRKS 303

RESULT 10
Q8C7I6 PRELIMINARY; PRT; 621 AA.
AC Q8C7I6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Mus musculus adult liver tumor cDNA, RIKEN full-length enriched
DE library, clone:C730023F16 product:hypothetical protein, full insert
DE sequence.
GN Name=1300002K09Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=103479636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,


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SQ SEQUENCE 621 AA; 71002 MW; 909E1C6BC2A9EA60 CRC64;
Query Match 7.8%; Score 133; DB 2; Length 621;
Best Local Similarity 23.1%; Pred. No. 0.025;
Matches 55; Conservative 37; Mismatches 92; Indels 54; Gaps 7;
QY 50 LAGLLVQOIIFFLGTALAFVLMPVLHGRNLLFFRSLESSWPFMTLALAV---ILQNM 106
DB 388 LWGLIHHVQSLGVMYGLVLPPIHHRGL---EMLOGFGLGVLTLSIVVGLLIQVM 444
QY 107 AAHWFELETHDHPQ-----LTNRRLVYAATFLFPLNLVGMAMXXKCSPSIAI----- 155
DB 445 IAGTFELQPKLGTSDKQKPLANRRRAFFNFYFLFFYNVLLG--LGACLSRLILSLIG 502
QY 156 -----RHPTPGYTYRNFLEKIEVSQSHPMATFACSLLLQAQSLPRTWA 199
DB 503 TWLIARIDRTIMOSYEGADMGAGWGLFVDHYHTNPVLSVFCILITS----- 553
QY 200 APQDSLRPGEDGCMOLLQTKDSMAKGARPG-AXRGRARWGLAYTLHLNPTLQVFRKT 256
DB 554 -----HKORKLQTYKVCNQSAGRPSARATRWFLQTLINPRLVWLKRS 602

RESULT 12
Q8PBV8 PRELIMINARY; PRT; 618 AA.
AC Q8PBV8
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Hypothetical protein XCC1009.
GN OrderedLocusNames=XCC1009.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral L.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Martins E.C., Moon D.H.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Tindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Stubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR EMBL; AE012197; AAM40309.1;
KW Complete proteome.
SQ SEQUENCE 618 AA; 67854 MW; 93B6E2A062AD6B69 CRC64;
Query Match 6.8%; Score 115.5; DB 2; Length 618;
Best Local Similarity 23.0%; Pred. No. 0.66;
Matches 90; Conservative 40; Mismatches 97; Indels 165; Gaps 22;
QY 3 ISALVLSCLTFLVLMBSLVTHRGSGSGDQPSWNLFSVPLPLPLAGLLVQOIIFFL 62
DB 246 IQAALVTPLLANAMKVSLAGTRAGSGS---RAQWRYF-----GLLG----- 285
QY 63 GTTALAFVLMPVLHGRNLLFFRSLES---SWPFMTLALAVILQNMAAHVFLETHDGH 119
DB 286 GISTLAIFVLG-----PFSDAERISPHWPLPGVLLALVAAVILMRW----- 327

us-09-816-653a-4.rup
QY 120 POLTNRRVLYAATFLFPLNLVGMAMXXKCSPSI-AIRHPTPG---YYTYRNF----- 168
DB 328 -----PRPLRRATWLIALGLML-GAYSYVLAVSPAIRAAAGEKYYP-RNFAGWKDLAR 380
QY 169 -LKIEVSQSHPMATFACSLLLQAQSLPRTWAPODSLPGSE-----DEGMQLLOT-- 219
DB 381 AVKTELAQPPG-----TRVLA---ENFKVGAEGLFQLHDAQIEVLQADL 422
QY 220 KDSMAKGARPGAXRGRARWGL-----AYTLHLNPTLQVFRK-----TALGA-- 261
DB 423 NDKGRSAQ-----LAQGLLSHGRSGPRLVLVSPDQRYRDLTLTRVHAICAMVGPLP 476
QY 262 -----NGAQ-----PCSSLPGSPSPSITPAM----- 281
DB 477 PPKVSTDHGYRFLFLFALPAQRQFG--PCIAPAAMAWIDTLPGLGVAATTTMQVRGWAQKD 534
QY 282 -----QAGPPDHGXKVEVCLHWE 300
DB 535 GVGLSRVELLVDRPAGRADYGTATLDVPRYWK 566

RESULT 13
Q7NYU4 PRELIMINARY; PRT; 572 AA.
AC Q7NYU4
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Probable periplasmic binding protein.
GN OrderedLocusNames=CV1178;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araribe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Griesard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.P.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manlio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento P.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Petrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seuneh H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -I- SIMILIARITY: Belongs to the bacterial extracellular solute-binding
CC protein family 5.
DR EMBL; AE016914; AQ58853.1;
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002345; Lipocalin.
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DR InterPro; IPR000914; SBP_bac.5.
DR InterPro; IPR00058; wing_hlx_dna_bnd.
DR Pfam; PF00496; SBP_bac.5; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 572 AA; 65364 MW; 937A150164700A29 CRC64;

Query Match      5.9%; Score 100.5; DB 2; Length 572;
Best Local Similarity 23.7%; Pred. No. 9.8;
Matches 64; Conservative 26; Mismatches 79; Indels 101; Gaps 14;

QY 17 LMRSLVTHRLGGSGDGFQSWNLSVPLPLPPLA-----GLLVQQLIFFLGTT 65
DB 122 LIASLPQH-LGAGDSG-----RSRIPLPHAPLPLDFQVRVARLESILVQIFDRLCRH 174

QY 66 ALAFVLVLPVL-----HGNNLFFRSLESSWPFWLTALAVILONNAHWFLETHD 117
DB 175 DRLGQVLRPALAHWEADPEGN-----WRFWLRPG-----LRFHD 210

QY 118 GHPOLTNRRVLVAATFLLPLNVLGMXXCSPSIATRHPTGYT-YRNFLKIEVSQS 176
DB 211 GGP-----LDAET-----AAASLLRLKQPDNPYHALYHLRRVDV--- 245

QY 177 HPAMTAFCSLLLOAQSLPRTWAAPODSLRLPCEDEGMQLLOTKDSMAKGARPGAXRGRA 236
DB 246 HDALSFSCR-LTEADHLWQRLATANASIVP-----MRSQDFERPMPVGSOPFEV--- 295

QY 237 RMGLAYTLHNPTL-----QVFRKTALL 259
DB 296 -----LHSPQLKLAAPFQHYRERALL 317

RESULT 14
Q7TNJ2 PRELIMINARY; PRT; 2170 AA.
AC Q7TNJ2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE ATP-binding cassette transporter sub-family A member 7.
GN Name=ABCA7;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Platelet;
RA Sasaki M., Nada S., Yamaguchi A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AB097814; BAC81426.1; -.
DR HSSP; P58301; 1P2T.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding.
SQ SEQUENCE 2170 AA; 237718 MW; 003C8DF70B8744CE CRC64;

Query Match      5.9%; Score 100; DB 2; Length 2170;
Best Local Similarity 23.7%; Pred. No. 46;
Matches 82; Conservative 62; Mismatches 124; Indels 78; Gaps 19;

QY 3 ISALVLSCL---LTF-----LVMRLSLVTH-----RLGGSGGD-----GQFSWNLFSVPL 45

DR InterPro; IPR000914; SBP_bac.5.
DR InterPro; IPR00058; wing_hlx_dna_bnd.
DR Pfam; PF00496; SBP_bac.5; 1.
DR PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 572 AA; 65364 MW; 937A150164700A29 CRC64;

Query Match      5.9%; Score 100.5; DB 2; Length 572;
Best Local Similarity 23.7%; Pred. No. 9.8;
Matches 64; Conservative 26; Mismatches 79; Indels 101; Gaps 14;

QY 17 LMRSLVTHRLGGSGDGFQSWNLSVPLPLPPLA-----GLLVQQLIFFLGTT 65
DB 122 LIASLPQH-LGAGDSG-----RSRIPLPHAPLPLDFQVRVARLESILVQIFDRLCRH 174

QY 66 ALAFVLVLPVL-----HGNNLFFRSLESSWPFWLTALAVILONNAHWFLETHD 117
DB 175 DRLGQVLRPALAHWEADPEGN-----WRFWLRPG-----LRFHD 210

QY 118 GHPOLTNRRVLVAATFLLPLNVLGMXXCSPSIATRHPTGYT-YRNFLKIEVSQS 176
DB 211 GGP-----LDAET-----AAASLLRLKQPDNPYHALYHLRRVDV--- 245

QY 177 HPAMTAFCSLLLOAQSLPRTWAAPODSLRLPCEDEGMQLLOTKDSMAKGARPGAXRGRA 236
DB 246 HDALSFSCR-LTEADHLWQRLATANASIVP-----MRSQDFERPMPVGSOPFEV--- 295

QY 237 RMGLAYTLHNPTL-----QVFRKTALL 259
DB 296 -----LHSPQLKLAAPFQHYRERALL 317

RESULT 15
Q9ER60 PRELIMINARY; PRT; 1841 AA.
AC Q9ER60;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel.
GN Name=Scn4a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=balb/c; TISSUE=Heart;
RA Zimmer T., Benndorf K.;
RT "The mouse heart sodium channel (mH1): cloning and characterization of alternatively spliced variants."
RT Am. J. Physiol. Heart Circ. Physiol. 282:H1007-H1017(2002).
CC -1- SURCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AJ278787; CAC17146.1; -.
DR HSSP; P04775; 1BYI.
DR MGD; MGI:98250; Scn4a.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008052; Na_channel4.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01665; NACHANNEL4.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS00966; IQ; 1.
KW Ion transport; Ionic channel; Sodium channel; Sodium transport;
KW Transmembrane; Transport; Voltage-gated channel.
SQ SEQUENCE 1841 AA; 208796 MW; 0766DFD33A9E0B55 CRC64;

Query Match      5.8%; Score 98.5; DB 2; Length 1841;
Best Local Similarity 22.0%; Pred. No. 51;
Matches 67; Conservative 35; Mismatches 105; Indels 97; Gaps 14;

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QY 35 QFSWNLFSVPLPLPLAGLLVQOIIFPLGTALAFVLVMPVLHGRNLLFFRSLESSWPEW 94
Db 633 QCGWNIFD-----SIVTSLVELG--LANVQGLSVLRSFLLRVFKLAKSWP-T 679
QY 95 LTLALAVILQNMMAHWVLETHDGHQPOLTNRRLVYAATFLLPPL--NVLVGAMXXXCSPS 152
Db 680 LNMLIKIIIGNSVGA-----LGNLTIVLAIIVFIFAVVGMQLFGKSYKECVCK 726
QY 153 IAIRHPTPGYTT---YRNFKI-----EVSQSHPAMTAFCSILLQQA-- 191
Db 727 IASDCSLPRWHMDFHSLIVFRILCGEWIETMWDCEVAGQAMCLTVFLVMVIGNLV 786
QY 192 -----SLLPRTMAAPQDSLPGEEDEGMOLLQTKDSMAKGPAGXRGARWGLAYT-- 243
Db 787 VLNLFLALLSSFSA--DSLAADEDEGMNNLQ-----IAIGRIKWGIAPAKT 832
QY 244 ----LHNPQLQVFRKTALL-----GANGAQCSSLPGSPPSITPAMQAGPPDHXG 291
Db 833 FLIGLHLHGKILSL--KDIMLSLGEPPGAGENGESP-----PEDEKKEPPPPEDG 878
QY 292 XVEV 295
Db 879 NKEL 882
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Search completed: February 8, 2005, 13:40:10
Job time : 145.653 secs

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